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GJE-65

SEQUENCE LISTING

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<120> VIRULENCE GENES AND PROTEINS, AND THEIR USE

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<170> PatentIn Ver. 2.1

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 Glu Gln Ala Leu Gly Asn Leu Leu Asp Asn Ala Ile Asp Phe Thr Pro
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 Glu Ser Gly Cys Ile Thr Leu Ser Ala Glu Val Asp Gln Glu Tyr Val
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 Thr Leu Lys Val Leu Asp Thr Gly Ser Gly Ile Pro Asp Tyr Ala Leu
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 Ser Arg Ile Phe Glu Arg Phe Tyr Ser Leu Pro Arg Ala Asn Gly Gln
 420 425 430
 Lys Ser Ser Gly Leu Gly Leu Ala Phe Val Ser Glu Val Ala Arg Leu
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 Val Gly Ala Ala Leu Ser Asn Lys Leu Ala Lys Ile Asn Leu His Thr
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 Thr Ala His Ala Asp Tyr Gln Cys Ser Val Thr Pro Arg Asp Asp Val
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Ile Val Ser Pro Gln Thr Val Gln Val Lys Gly Glu Asn Gly Asn Leu	
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Val Ile Thr Pro Asp Gly Asn Val Met Tyr Asn Gly Lys Gln Tyr Ser	
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65 70 75 80	
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Arg Ser Thr Leu Pro Trp Ile Asp Gly Gly Ala Lys Ser Arg Val Glu	
85 90 95	
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Lys Ala Arg Ile Ala Leu Asp Lys Ile Ile Val Gln Glu Met Gly Glu	
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Ser Ser Lys Met Arg Ser Arg Leu Thr Lys Leu Asp Ala Gln Leu Lys	
115 120 125	
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Glu Gln Met Asn Arg Ile Ile Glu Thr Arg Ser Asp Gly Leu Thr Phe	
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145 150 155 160	
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Asn Gln Ala Met Gly Gly Ile Leu Gln Asp Ser Ile Asn Glu Met Gly	
165 170 175	
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Gly Ser Leu Gly Gly Leu Gln Ser Ser Ile Gln Thr Glu Trp Lys Lys	
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Gln Glu Lys Asp Phe Gln Gln Phe Gly Lys Asp Val Cys Ser Arg Val	
210 215 220	
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Val Thr Leu Glu Asp Ser Arg Lys Ala Leu Val Gly Asn Leu Lys	
225 230 235	

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Glu	Gln	Met	Asn	Arg	Ile	Ile	Glu	Thr	Arg	Ser	Asp	Gly	Leu	Thr	Phe
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Phe Gly Thr Lys Lys Leu Gly Ser Ile Gly Ser Asp Leu Gly Ala Ser
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Ile Lys Gly Phe Lys Lys Ala Met Ser Asp Asp Glu Pro Lys Gln Asp
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Lys Thr Ser Gln Asp Ala Asp Phe Thr Ala Lys Thr Ile Ala Asp Lys
      55                60                65

cag gcg gat acg aat cag gaa cag gct aaa ata gaa gac gcg aag cgc 1255
Gln Ala Asp Thr Asn Gln Glu Gln Ala Lys Ile Glu Asp Ala Lys Arg
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cac gat aaa gag cag gtg taa tct gtg ttt gat atc ggt ttt agc gaa 1303
His Asp Lys Glu Gln Val          Val Phe Asp Ile Gly Phe Ser Glu
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Leu Pro Val Ala Val Lys Thr Val Ala Gly Trp Ile Arg Ala Leu Arg
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Gln Glu Phe Gln Asp Ser Leu Lys Lys Val Glu Lys Ala Ser Leu Thr	
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260 265 270	
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Leu Ile Glu Leu Arg Lys Arg Leu Leu Asn Cys Ile Ile Ser Val Ile	
275 280 285	
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Gln Lys Leu Ala Arg Gln Tyr Ser Ser Cys Trp Ser Thr Ala Gly Val	
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Phe Val Ala Gln Leu Arg Ile Ala Ala Glu Leu Asn Met Pro Val Phe	
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Gly Ala Ser Ile Lys Gly Phe Lys Lys Ala Met Ser Asp Asp Glu Pro
 35 40 45

Lys Gln Asp Lys Thr Ser Gln Asp Ala Asp Phe Thr Ala Lys Thr Ile
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Ala Gly Trp Ile Arg Ala Leu Arg Ser Leu Ala Thr Thr Val Gln Asn

35 40 45
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 Lys Val Glu Lys Ala Ser Leu Thr Asn Leu Thr Pro Glu Leu Lys Ala
 65 70 75 80
 Ser Met Asp Glu Leu Arg Gln Ala Ala Glu Ser Met Lys Arg Ser Tyr
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 Val Ala Asn Asp Pro Glu Lys Ala Ser Asp Glu Ala His Thr Ile His
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 Asn Pro Val Val Lys Asp Asn Glu Thr Ala His Glu Gly Val Thr Pro
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Pro Ala Leu Tyr Lys His Glu Arg Arg Leu Val Val Pro Leu Leu Val
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Val Gln Val Ser Thr Asp Ile Ala Ser Tyr Leu Ser Phe Val Met Ala
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Arg Pro Tyr Val Leu Val Gly Ala Phe Val Val Gly Met Leu Leu Thr
 195 200 205

Pro Pro Asp Val Phe Ser Gln Thr Leu Leu Ala Ile Pro Met Tyr Cys
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 Gly Leu Asp Phe Asn Arg Asn Phe Ser Thr Pro Glu Glu Gln Glu Arg
 100 105 110
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 tggtttttaa ggcgcgttct gttgccggtt atatgtcaag aaggatatct atg ggt gag 178
 Met Gly Glu
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att agt att acc aaa ctg ctg gta gtt gcg gcg ctg gtc gtt ctg ctg 226
 Ile Ser Ile Thr Lys Leu Leu Val Val Ala Ala Leu Val Val Leu Leu
 5 10 15

ttt ggg act aag aag tta cgt acg ctg ggc gga gac ctt gga gcg gcc 274
 Phe Gly Thr Lys Lys Leu Arg Thr Leu Gly Gly Asp Leu Gly Ala Ala
 20 25 30 35

att aaa ggg ttc aag aag gcg atg aat gat gac gat gct gcg gcg aaa 322
 Ile Lys Gly Phe Lys Lys Ala Met Asn Asp Asp Asp Ala Ala Ala Lys
 40 45 50

aaa ggc gca gac gtt gat ctt cag gct gaa aag ctc tct cat aaa gag 370
 Lys Gly Ala Asp Val Asp Leu Gln Ala Glu Lys Leu Ser His Lys Glu
 55 60 65

tgacgtggcg agcaggacgc tccctcaata tcttgttcga tacaaaaacc cgcttcaaaa 430

agcggggttt ttatcagaca gatgtaagta attattacag gattacttaa cttccatccc 490

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aaagcccatc gccagcgctt cgctttcatt tcgtcg 586

<210> 16

<211> 67

<212> PRT

<213> Escherichia coli

<400> 16

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 1 5 10 15

Val Leu Leu Phe Gly Thr Lys Lys Leu Arg Thr Leu Gly Gly Asp Leu
 20 25 30

Gly Ala Ala Ile Lys Gly Phe Lys Lys Ala Met Asn Asp Asp Asp Ala
 35 40 45

Ala Ala Lys Lys Gly Ala Asp Val Asp Leu Gln Ala Glu Lys Leu Ser
 50 55 60

His Lys Glu
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<210> 17
<211> 4200
<212> DNA
<213> Salmonella typhimurium

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<222> (1450) .. (1722)

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cgctgttgt cgaatcttcc ccctcgtcga gtgataaacc gtaaac atg gct gta 955
Met Ala Val

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gaa gat act caa ccg ctt atc acg cat ctg atc gag ttg cgt aag cgc	1003
Glu Asp Thr Gln Pro Leu Ile Thr His Leu Ile Glu Leu Arg Lys Arg	
5 10 15	
ctg cta aac tgc atc gtc gca gta ctt ctg att ttt ctg gcg tta att	1051
Leu Leu Asn Cys Ile Val Ala Val Leu Leu Ile Phe Leu Ala Leu Ile	
20 25 30 35	
tat ttc gcc aat gat att tat cat tta gtc gcc gca ccg ctg att aaa	1099
Tyr Phe Ala Asn Asp Ile Tyr His Leu Val Ala Ala Pro Leu Ile Lys	
40 45 50	
cag atg ccg caa ggg gcg aca atg att gcg acg gat gtg gcg tcg ccg	1147
Gln Met Pro Gln Gly Ala Thr Met Ile Ala Thr Asp Val Ala Ser Pro	
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70 75 80	
gcg cct gtc att ttg tac cag gtt tgg gcc ttt atc gcc ccg gcg ctg	1243
Ala Pro Val Ile Leu Tyr Gln Val Trp Ala Phe Ile Ala Pro Ala Leu	
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Tyr Lys His Glu Arg Arg Leu Val Val Pro Leu Leu Val Ser Ser Ser	
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Leu Ala Phe Gly Phe Leu Thr His Thr Ala Pro Glu Gly Val Gln Val	
135 140 145	
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Ser Thr Asp Ile Ala Ser Tyr Leu Ser Phe Val Met Ala Leu Phe Met	
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gcc ttt gcg tagcc ttt gaa gtg ccg gtg gcg att gtg ttg ctg tgc tgg	1485
Ala Phe Ala Phe Glu Val Pro Val Ala Ile Val Leu Leu Cys Trp	
165 170 175	
atg ggc atc acc acg cca gaa gat ttg cgt aaa aaa cgg cct tat atc	1533
Met Gly Ile Thr Thr Pro Glu Asp Leu Arg Lys Lys Arg Pro Tyr Ile	
180 185 190	
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<210> 18

<211> 166

<212> PRT

<213> Salmonella typhimurium

<400> 18

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Ala Leu Ile Tyr Phe Ala Asn Asp Ile Tyr His Leu Val Ala Ala Pro
 35 40 45

Leu Ile Lys Gln Met Pro Gln Gly Ala Thr Met Ile Ala Thr Asp Val
 50 55 60

Ala Ser Pro Phe Phe Thr Pro Ile Lys Leu Thr Phe Met Val Ser Leu
 65 70 75 80

Ile Leu Ser Ala Pro Val Ile Leu Tyr Gln Val Trp Ala Phe Ile Ala
 85 90 95

Pro Ala Leu Tyr Lys His Glu Arg Arg Leu Val Val Pro Leu Leu Val
 100 105 110

Ser Ser Ser Leu Leu Phe Tyr Ile Gly Met Ala Phe Ala Tyr Phe Val
 115 120 125

Val Phe Pro Leu Ala Phe Gly Phe Leu Thr His Thr Ala Pro Glu Gly
 130 135 140

Val Gln Val Ser Thr Asp Ile Ala Ser Tyr Leu Ser Phe Val Met Ala
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Leu Phe Met Ala Phe Ala
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<210> 19

<211> 91

<212> PRT

<213> Salmonella typhimurium

<400> 19

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Thr Pro Glu Asp Leu Arg Lys Lys Arg Pro Tyr Ile Leu Val Gly Ala
 20 25 30

Phe Ile Val Gly Met Leu Leu Thr Pro Pro Asp Val Phe Ser Gln Thr

35	40	45
Leu Leu Ala Ile Pro Met Tyr Cys Leu Phe Glu Ile Gly Val Phe Cys		
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<210> 20
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 <212> DNA
 <213> *Neisseria meningitidis*

<220>
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 <222> (1572)..(2339)

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 aaaatgatgc tgaaagtcc cgaaatcgcc aaagcggcag gactggcaga cggcttcaaa 540
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 catcatgggc agtttttctc tgacgcactg gattatcgta ctgattatcg tcgttttgat 720
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                Val Ser Glu Thr Gln Asn Glu Gln Pro Val Gln Pro Leu
                  1             5             10

gtc gag cat ctc atc gag ctg cgc cgc cgc ctg atg tgg acg gtt gtc 1658
Val Glu His Leu Ile Glu Leu Arg Arg Arg Leu Met Trp Thr Val Val
    15             20             25

ggg atc tta gtc tgc ttt ttc ggc cta atg ccg ttt gcc caa caa ctc 1706
Gly Ile Leu Val Cys Phe Phe Gly Leu Met Pro Phe Ala Gln Gln Leu
    30             35             40             45

tat act ttt atc gcc gac ccg ctg atg gca aac ctg ccc aaa gac acc 1754
Tyr Thr Phe Ile Ala Asp Pro Leu Met Ala Asn Leu Pro Lys Asp Thr
    50             55             60

agc atg att gcc acc gat gtc atc gca cca ttt ttc gtg ccg gtc aaa 1802
Ser Met Ile Ala Thr Asp Val Ile Ala Pro Phe Phe Val Pro Val Lys
    65             70             75

gtt acc ctg atg gcg gca ttt tta att tcg ctg ccg cat acg ctc tac 1850
Val Thr Leu Met Ala Ala Phe Leu Ile Ser Leu Pro His Thr Leu Tyr
    80             85             90

caa atc tgg gca ttc gtc gcc ccc gca ctc tac caa aac gaa aaa cgc 1898
Gln Ile Trp Ala Phe Val Ala Pro Ala Leu Tyr Gln Asn Glu Lys Arg
    95             100            105

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ctg att acg ccg ctc gtc ctc tcc agc gtc agc ctg ttt ttc atc ggc 1946
Leu Ile Thr Pro Leu Val Leu Ser Ser Val Ser Leu Phe Phe Ile Gly
110          115          120          125

atg gca ttt gcc tac ttt ttg gtt ttc ccc gtc att ttc aaa ttc ctt 1994
Met Ala Phe Ala Tyr Phe Leu Val Phe Pro Val Ile Phe Lys Phe Leu
          130          135          140

gcc agc gtt acc cct gtc ggt gtc aat atg gcg aca gac atc gac aaa 2042
Ala Ser Val Thr Pro Val Gly Val Asn Met Ala Thr Asp Ile Asp Lys
          145          150          155

tac ctc tcc ttc atc ttg ggg atg ttt gtc gca ttc ggt aca acg ttt 2090
Tyr Leu Ser Phe Ile Leu Gly Met Phe Val Ala Phe Gly Thr Thr Phe
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gaa gtc ccc att gtc gtt atc ctg tta acc aaa att ggt gtg gta aca 2138
Glu Val Pro Ile Val Val Ile Leu Leu Thr Lys Ile Gly Val Val Thr
          175          180          185

acc gaa cag ctc aaa cgc gcc cgc ccc tat gtg att gtc ggc gcg ttt 2186
Thr Glu Gln Leu Lys Arg Ala Arg Pro Tyr Val Ile Val Gly Ala Phe
190          195          200          205

gtc att gcc gcc atc atc acg ccg ccc gat gtg att tca caa acc ctg 2234
Val Ile Ala Ala Ile Ile Thr Pro Pro Asp Val Ile Ser Gln Thr Leu
          210          215          220

ctt gcc att ccg ctg att ctc tta tac gaa gca ggt att tgg ttc gga 2282
Leu Ala Ile Pro Leu Ile Leu Leu Tyr Glu Ala Gly Ile Trp Phe Gly
          225          230          235

cgc ttt ttc acg cca cgt tca gaa cag gat ggc gac ata cag ccg cct 2330
Arg Phe Phe Thr Pro Arg Ser Glu Gln Asp Gly Asp Ile Gln Pro Pro
          240          245          250

gca aca acc tgacactatg ccgtccgaac ctccgcctca taccgccaca 2379
Ala Thr Thr
255

gattaaggaa tacctttgaa taccctctat ttaggttcaa acagcccgcg ccgaatggaa 2439

atcctgacac agttgggcta tcaggctcgtc aagctgcctg ccaacatcga cgaaacggtc 2499

agacagaacg aagaccctgc ccgttacgtt caaaggatgg cagaagaaaa aaaccgaacc 2559

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<210> 21

<211> 256

<212> PRT

<213> Neisseria meningitidis

<400> 21

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			20				25						30		
Val	Cys	Phe	Phe	Gly	Leu	Met	Pro	Phe	Ala	Gln	Gln	Leu	Tyr	Thr	Phe
		35				40						45			
Ile	Ala	Asp	Pro	Leu	Met	Ala	Asn	Leu	Pro	Lys	Asp	Thr	Ser	Met	Ile
	50					55					60				
Ala	Thr	Asp	Val	Ile	Ala	Pro	Phe	Phe	Val	Pro	Val	Lys	Val	Thr	Leu
65					70					75					80
Met	Ala	Ala	Phe	Leu	Ile	Ser	Leu	Pro	His	Thr	Leu	Tyr	Gln	Ile	Trp
				85					90					95	
Ala	Phe	Val	Ala	Pro	Ala	Leu	Tyr	Gln	Asn	Glu	Lys	Arg	Leu	Ile	Thr
			100					105					110		
Pro	Leu	Val	Leu	Ser	Ser	Val	Ser	Leu	Phe	Phe	Ile	Gly	Met	Ala	Phe
		115					120					125			
Ala	Tyr	Phe	Leu	Val	Phe	Pro	Val	Ile	Phe	Lys	Phe	Leu	Ala	Ser	Val
	130					135					140				
Thr	Pro	Val	Gly	Val	Asn	Met	Ala	Thr	Asp	Ile	Asp	Lys	Tyr	Leu	Ser
145					150					155					160
Phe	Ile	Leu	Gly	Met	Phe	Val	Ala	Phe	Gly	Thr	Thr	Phe	Glu	Val	Pro
			165						170					175	
Ile	Val	Val	Ile	Leu	Leu	Thr	Lys	Ile	Gly	Val	Val	Thr	Thr	Glu	Gln
			180					185						190	
Leu	Lys	Arg	Ala	Arg	Pro	Tyr	Val	Ile	Val	Gly	Ala	Phe	Val	Ile	Ala
		195					200					205			
Ala	Ile	Ile	Thr	Pro	Pro	Asp	Val	Ile	Ser	Gln	Thr	Leu	Leu	Ala	Ile
	210					215					220				
Pro	Leu	Ile	Leu	Leu	Tyr	Glu	Ala	Gly	Ile	Trp	Phe	Gly	Arg	Phe	Phe
225					230					235					240
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<210> 22
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<220>
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 Ser Leu Ile Lys Tyr Ser Glu Thr Asp Tyr Thr Ile Tyr Cys Asp Gln
 20 25 30
 gat gat att tgg tta gaa aac aaa ata ttt gaa tta gta aag tat gca 146
 Asp Asp Ile Trp Leu Glu Asn Lys Ile Phe Glu Leu Val Lys Tyr Ala
 35 40 45
 aat gaa att aaa ttg aat gta tca gat gcg cct tcg cta gtt tat gct 194
 Asn Glu Ile Lys Leu Asn Val Ser Asp Ala Pro Ser Leu Val Tyr Ala
 50 55 60
 gat ggc tat gct tat atg gat ggt gag ggt aca atc gat ttt tct ggg 242
 Asp Gly Tyr Ala Tyr Met Asp Gly Glu Gly Thr Ile Asp Phe Ser Gly
 65 70 75
 ata tct aac aat cat gct gat caa tta aag gat ttt ctt ttt ttt aat 290
 Ile Ser Asn Asn His Ala Asp Gln Leu Lys Asp Phe Leu Phe Phe Asn
 80 85 90 95
 ggt gga tac caa gga tgt tct att atg ttc aat cgt gca atg acc aaa 338
 Gly Gly Tyr Gln Gly Cys Ser Ile Met Phe Asn Arg Ala Met Thr Lys
 100 105 110

ttt ctt ctg aat tat cga gga ttt gta tat cta cat gac gat atc aca	386
Phe Leu Leu Asn Tyr Arg Gly Phe Val Tyr Leu His Asp Asp Ile Thr	
115 120 125	
aca tta gct gca tac gct ctt ggt aaa gtt tat ttt ctc ccg aaa tac	434
Thr Leu Ala Ala Tyr Ala Leu Gly Lys Val Tyr Phe Leu Pro Lys Tyr	
130 135 140	
ctt atg tta tat aga cag cac acg aat gcg gta act ggt atc aaa aca	482
Leu Met Leu Tyr Arg Gln His Thr Asn Ala Val Thr Gly Ile Lys Thr	
145 150 155	
ttc cgc aat gga ttg act tct aaa ttt aaa tca cca gta aac tat ctt	530
Phe Arg Asn Gly Leu Thr Ser Lys Phe Lys Ser Pro Val Asn Tyr Leu	
160 165 170 175	
tta tca cga aaa cat tat cag gta aaa aaa tct ttt ttt gaa tgt aac	578
Leu Ser Arg Lys His Tyr Gln Val Lys Lys Ser Phe Phe Glu Cys Asn	
180 185 190	
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Ser Ser Ile Leu Ser Glu Thr Asn Lys Lys Val Phe Leu Asp Phe Ile	
195 200 205	
tca ttt tgt gaa tca aat aat aaa ttt aca gat ttt ttt aag tta tgg	674
Ser Phe Cys Glu Ser Asn Asn Lys Phe Thr Asp Phe Phe Lys Leu Trp	
210 215 220	
cga ggt ggg ttt aga tta aat aac agt aga act aaa tta tta tta aaa	722
Arg Gly Gly Phe Arg Leu Asn Asn Ser Arg Thr Lys Leu Leu Leu Lys	
225 230 235	
ttc tta ata cgg aga aaa ttt agc ga atg att tca ata ctt aca cct	769
Phe Leu Ile Arg Arg Lys Phe Ser Met Ile Ser Ile Leu Thr Pro	
240 245 250	
act ttt aat cgg caa cat act tta tca agg cta ttc aat tct ctt ata	817
Thr Phe Asn Arg Gln His Thr Leu Ser Arg Leu Phe Asn Ser Leu Ile	
255 260 265 270	
tta caa act gat aaa gat ttt gag tgg ata ata att gat gat ggt agt	865
Leu Gln Thr Asp Lys Asp Phe Glu Trp Ile Ile Ile Asp Asp Gly Ser	
275 280 285	
ata gat gca aca gcg gta ctt gta gaa gat ttt aga aaa aaa tgt gat	913
Ile Asp Ala Thr Ala Val Leu Val Glu Asp Phe Arg Lys Lys Cys Asp	
290 295 300	
ttt gac ttg att tat tgc tat cag gaa aat aat ggt aag ccc atg gct	961
Phe Asp Leu Ile Tyr Cys Tyr Gln Glu Asn Asn Gly Lys Pro Met Ala	
305 310 315	

tta aac gct ggt gtt aaa gct tgt aga ggc gat tat atc ttt att gtt	1009
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320 325 330	
gac agt gat gat gca cta act ccc gat gcc ata aaa tta att aaa gaa	1057
Asp Ser Asp Asp Ala Leu Thr Pro Asp Ala Ile Lys Leu Ile Lys Glu	
335 340 345 350	
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Ser Ile His Asp Cys Leu Ser Glu Lys Glu Ser Phe Ser Gly Val Gly	
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Phe Arg Lys Ala Tyr Ile Lys Gly Gly Ile Ile Gly Asn Asp Leu Asn	
370 375 380	
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Asn Ser Ser Glu His Ile Tyr Tyr Leu Asn Ala Thr Glu Ile Ser Asn	
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Leu Ile Asn Gly Asp Val Ala Tyr Cys Phe Lys Lys Glu Ser Leu Val	
400 405 410	
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Lys Asn Pro Phe Pro Arg Ile Glu Asp Glu Lys Phe Val Pro Glu Leu	
415 420 425 430	
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Tyr Ile Trp Asn Lys Ile Thr Asp Lys Ala Lys Ile Arg Phe Asn Ile	
435 440 445	
agc aaa gtt ata tat ctt tgt gag tat ctt gat gat ggt ctt tct aaa	1393
Ser Lys Val Ile Tyr Leu Cys Glu Tyr Leu Asp Asp Gly Leu Ser Lys	
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Asn Phe His Asn Gln Leu Lys Lys Tyr Pro Lys Gly Phe Lys Ile Tyr	
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Tyr Lys Asp Gln Arg Lys Arg Glu Lys Thr Tyr Ile Lys Lys Thr Lys	
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atg cta att aga tat ttg caa tgt tgt tat tat gag aaa ata aa atg	1536
Met Leu Ile Arg Tyr Leu Gln Cys Cys Tyr Tyr Glu Lys Ile Met	
495 500 505	
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Lys Ile Leu Phe Val Ile Thr Gly Leu Gly Leu Gly Gly Ala Glu Lys	
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Gln Val Cys Leu Leu Ala Asp Lys Leu Ser Leu Ser Gly His His Val	
530 535 540	
aag att att tca ctt gga cat atg tct aat aat aaa gtc ttt cct agc	1680
Lys Ile Ile Ser Leu Gly His Met Ser Asn Asn Lys Val Phe Pro Ser	
545 550 555	
gaa aat aat gtt aat gtc att aat gta aat atg tca aaa aac att tct	1728
Glu Asn Asn Val Asn Val Ile Asn Val Asn Met Ser Lys Asn Ile Ser	
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gga gtt ata aaa ggt tgt gtc aga att aga gat gtt ata gct aat ttc	1776
Gly Val Ile Lys Gly Cys Val Arg Ile Arg Asp Val Ile Ala Asn Phe	
575 580 585	
aaa cca gac att gta cac agt cat atg ttt cat gca aac att atc act	1824
Lys Pro Asp Ile Val His Ser His Met Phe His Ala Asn Ile Ile Thr	
590 595 600 605	
aga ttg tct gta att gga atc aaa aac aga cct ggt att ata tca act	1872
Arg Leu Ser Val Ile Gly Ile Lys Asn Arg Pro Gly Ile Ile Ser Thr	
610 615 620	
gca cat aat aaa aat gaa ggt ggg tat ttc aga atg ctc aca tat aga	1920
Ala His Asn Lys Asn Glu Gly Gly Tyr Phe Arg Met Leu Thr Tyr Arg	
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ata acc gat tgt tta agt gat tgt tgt aca aat gtt agc aaa gaa gca	1968
Ile Thr Asp Cys Leu Ser Asp Cys Cys Thr Asn Val Ser Lys Glu Ala	
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gtg gat gag ttt tta cgg ata aaa gcc ttt aat ccc gct aaa gca att	2016
Val Asp Glu Phe Leu Arg Ile Lys Ala Phe Asn Pro Ala Lys Ala Ile	
655 660 665	
act atg tat aat ggg ata gat acc aat aaa ttt aaa ttt gat tta ttg	2064
Thr Met Tyr Asn Gly Ile Asp Thr Asn Lys Phe Lys Phe Asp Leu Leu	
670 675 680 685	
gca agg agg gaa att cga gac ggt att aat ata aaa aat gat gat ata	2112
Ala Arg Arg Glu Ile Arg Asp Gly Ile Asn Ile Lys Asn Asp Asp Ile	
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Leu Leu Leu Ala Ala Gly Arg Leu Thr Leu Ala Lys Asp Tyr Pro Asn	
705 710 715	
tta ttg aat gca atg act ctg ctt cct gaa cac ttt aaa ctt att att	2208
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 735 740 745

ttg caa tta tct aat agg gtg tcc ttg ttg gga gtt aaa aaa aat att 2304
 Leu Gln Leu Ser Asn Arg Val Ser Leu Leu Gly Val Lys Lys Asn Ile
 750 755 760 765

gct ccc tat ttt tct gca tgt gat att ttt gtt ctc tct tct cgt tgg 2352
 Ala Pro Tyr Phe Ser Ala Cys Asp Ile Phe Val Leu Ser Ser Arg Trp
 770 775 780

gaa gga ttt gga tta gtc gtg gca gaa gct atg tca tgt gag cga att 2400
 Glu Gly Phe Gly Leu Val Val Ala Glu Ala Met Ser Cys Glu Arg Ile
 785 790 795

gtt gtt ggc acg gat tca ggg gga gta aga gaa gtt att ggt gac gat 2448
 Val Val Gly Thr Asp Ser Gly Gly Val Arg Glu Val Ile Gly Asp Asp
 800 805 810

gat ttt ctt gta ccc ata tct gat tca aca caa ctt gca agc aaa att 2496
 Asp Phe Leu Val Pro Ile Ser Asp Ser Thr Gln Leu Ala Ser Lys Ile
 815 820 825

gaa aaa ttg tct ttg agc cag ata cgt gat cac att ggt ttt cgg aat 2544
 Glu Lys Leu Ser Leu Ser Gln Ile Arg Asp His Ile Gly Phe Arg Asn
 830 835 840 845

cgt gag cgt att tta aaa aat ttc tca ata gat act att att atg cag 2592
 Arg Glu Arg Ile Leu Lys Asn Phe Ser Ile Asp Thr Ile Ile Met Gln
 850 855 860

tgg caa gaa ctc tat gga act ata att tgc tca aaa cat gaa agg 2637
 Trp Gln Glu Leu Tyr Gly Thr Ile Ile Cys Ser Lys His Glu Arg
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 Met Thr Ala Arg
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aca act aaa gtt ttg cac tta caa tta ctc cca ctc tta agt ggc gtt 3041

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Gln Arg Val Thr Leu Asn Glu Ile Ser Ala Leu Tyr Thr Asp Tyr Asp	
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Tyr Thr Leu Val Cys Ser Lys Lys Gly Pro Leu Thr Lys Ala Leu Leu	
915 920 925	
gaa tat gat gtc gat tgt cat tgt atc ccc gaa ctt acg aga gaa att	3185
Glu Tyr Asp Val Asp Cys His Cys Ile Pro Glu Leu Thr Arg Glu Ile	
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acc gta aag aat gat ttt aaa gca ttg ttc aag ctt tat aag ttc ata	3233
Thr Val Lys Asn Asp Phe Lys Ala Leu Phe Lys Leu Tyr Lys Phe Ile	
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Lys Lys Glu Lys Phe Asp Ile Val His Thr His Ser Ser Lys Thr Gly	
965 970 975	
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Ile Leu Gly Arg Val Ala Ala Lys Leu Ala Arg Val Gly Lys Val Ile	
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cac act gta cat ggt ttt tct ttt cca gcc gca tct agt aaa aaa agt	3377
His Thr Val His Gly Phe Ser Phe Pro Ala Ala Ser Ser Lys Lys Ser	
995 1000 1005	
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Tyr Tyr Leu Tyr Phe Phe Met Glu Trp Ile Ala Lys Phe Phe Thr Asp	
1010 1015 1020	
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Lys Leu Ile Val Leu Asn Val Asp Asp Glu Tyr Ile Ala Ile Asn Lys	
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tta aaa ttc aag cgg gat aaa gtt ttt tta att cct aat gga gta gac	3521
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1045 1050 1055	
act gat aag ttt tct cct tta gaa aat aaa att tat agt agc acc ttg	3569
Thr Asp Lys Phe Ser Pro Leu Glu Asn Lys Ile Tyr Ser Ser Thr Leu	
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aat cta gta atg gtt ggt aga tta tcc aag caa aaa gat cct gag aca	3617
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 1090 1095 1100

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 1140 1145 1150

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 Trp Glu Gly Met Pro Leu Ala Ile Leu Glu Ala Leu Ser Cys Gly Leu
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cca tgt ata gtc act aat att cca ggt aat aat agc tta ata gaa gat 3905
 Pro Cys Ile Val Thr Asn Ile Pro Gly Asn Asn Ser Leu Ile Glu Asp
 1170 1175 1180

ggc tat aat ggt tgt ttg ttt gaa att aga gat tgt cag tta tta tct 3953
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caa aaa atc atg tca tat gtt ggt aag cca gaa ctg att gca cag caa 4001
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tct acc aat gca cga tca ttt att ctg aaa aat tat gga tta gtt aaa 4049
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 1220 1225 1230

aga aat aat aag gtc aga cag cta tat gat aat taaatgaaac cgaaaagtta 4102
 Arg Asn Asn Lys Val Arg Gln Leu Tyr Asp Asn
 1235 1240

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cgtaacatct gcattacatt caagccgcac aaccccgcgg tgaccacccc tgacaggagt 4222

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cgctcaacat cgaaagccgt gggtataccg tctctatttt caaccgttcc cgtgaaaaga 4342

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 35 40 45
 Glu Ile Lys Leu Asn Val Ser Asp Ala Pro Ser Leu Val Tyr Ala Asp
 50 55 60
 Gly Tyr Ala Tyr Met Asp Gly Glu Gly Thr Ile Asp Phe Ser Gly Ile
 65 70 75 80
 Ser Asn Asn His Ala Asp Gln Leu Lys Asp Phe Leu Phe Phe Asn Gly
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 Gly Tyr Gln Gly Cys Ser Ile Met Phe Asn Arg Ala Met Thr Lys Phe
 100 105 110
 Leu Leu Asn Tyr Arg Gly Phe Val Tyr Leu His Asp Asp Ile Thr Thr
 115 120 125
 Leu Ala Ala Tyr Ala Leu Gly Lys Val Tyr Phe Leu Pro Lys Tyr Leu
 130 135 140
 Met Leu Tyr Arg Gln His Thr Asn Ala Val Thr Gly Ile Lys Thr Phe
 145 150 155 160
 Arg Asn Gly Leu Thr Ser Lys Phe Lys Ser Pro Val Asn Tyr Leu Leu
 165 170 175
 Ser Arg Lys His Tyr Gln Val Lys Lys Ser Phe Phe Glu Cys Asn Ser
 180 185 190
 Ser Ile Leu Ser Glu Thr Asn Lys Lys Val Phe Leu Asp Phe Ile Ser
 195 200 205

Phe Cys Glu Ser Asn Asn Lys Phe Thr Asp Phe Phe Lys Leu Trp Arg
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Leu Ile Arg Arg Lys Phe Ser
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<213> Escherichia coli

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Ile Ile Ile Asp Asp Gly Ser Ile Asp Ala Thr Ala Val Leu Val Glu
 35 40 45

Asp Phe Arg Lys Lys Cys Asp Phe Asp Leu Ile Tyr Cys Tyr Gln Glu
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Asn Asn Gly Lys Pro Met Ala Leu Asn Ala Gly Val Lys Ala Cys Arg
 65 70 75 80

Gly Asp Tyr Ile Phe Ile Val Asp Ser Asp Asp Ala Leu Thr Pro Asp
 85 90 95

Ala Ile Lys Leu Ile Lys Glu Ser Ile His Asp Cys Leu Ser Glu Lys
 100 105 110

Glu Ser Phe Ser Gly Val Gly Phe Arg Lys Ala Tyr Ile Lys Gly Gly
 115 120 125

Ile Ile Gly Asn Asp Leu Asn Asn Ser Ser Glu His Ile Tyr Tyr Leu
 130 135 140

Asn Ala Thr Glu Ile Ser Asn Leu Ile Asn Gly Asp Val Ala Tyr Cys
 145 150 155 160

Phe Lys Lys Glu Ser Leu Val Lys Asn Pro Phe Pro Arg Ile Glu Asp
 165 170 175

Glu Lys Phe Val Pro Glu Leu Tyr Ile Trp Asn Lys Ile Thr Asp Lys
 180 185 190

Ala Lys Ile Arg Phe Asn Ile Ser Lys Val Ile Tyr Leu Cys Glu Tyr
 195 200 205

Leu Asp Asp Gly Leu Ser Lys Asn Phe His Asn Gln Leu Lys Lys Tyr
 210 215 220

Pro Lys Gly Phe Lys Ile Tyr Tyr Lys Asp Gln Arg Lys Arg Glu Lys
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Tyr Tyr Glu Lys Ile
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<213> Escherichia coli

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Val Lys Ile Ile Ser Leu Gly His Met Ser Asn Asn Lys Val Phe Pro
 35 40 45

Ser Glu Asn Asn Val Asn Val Ile Asn Val Asn Met Ser Lys Asn Ile
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Ser Gly Val Ile Lys Gly Cys Val Arg Ile Arg Asp Val Ile Ala Asn
 65 70 75 80

Phe Lys Pro Asp Ile Val His Ser His Met Phe His Ala Asn Ile Ile
 85 90 95

Thr Arg Leu Ser Val Ile Gly Ile Lys Asn Arg Pro Gly Ile Ile Ser
 100 105 110

Thr Ala His Asn Lys Asn Glu Gly Gly Tyr Phe Arg Met Leu Thr Tyr
 115 120 125

Arg Ile Thr Asp Cys Leu Ser Asp Cys Cys Thr Asn Val Ser Lys Glu
 130 135 140

Ala Val Asp Glu Phe Leu Arg Ile Lys Ala Phe Asn Pro Ala Lys Ala
 145 150 155 160

Ile Thr Met Tyr Asn Gly Ile Asp Thr Asn Lys Phe Lys Phe Asp Leu
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 Leu Ala Arg Arg Glu Ile Arg Asp Gly Ile Asn Ile Lys Asn Asp Asp
 180 185 190
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 195 200 205
 Asn Leu Leu Asn Ala Met Thr Leu Leu Pro Glu His Phe Lys Leu Ile
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 Ile Ile Gly Asp Gly Glu Leu Arg Asp Glu Ile Asn Met Leu Ile Lys
 225 230 235 240
 Lys Leu Gln Leu Ser Asn Arg Val Ser Leu Leu Gly Val Lys Lys Asn
 245 250 255
 Ile Ala Pro Tyr Phe Ser Ala Cys Asp Ile Phe Val Leu Ser Ser Arg
 260 265 270
 Trp Glu Gly Phe Gly Leu Val Val Ala Glu Ala Met Ser Cys Glu Arg
 275 280 285
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 Asp Asp Phe Leu Val Pro Ile Ser Asp Ser Thr Gln Leu Ala Ser Lys
 305 310 315 320
 Ile Glu Lys Leu Ser Leu Ser Gln Ile Arg Asp His Ile Gly Phe Arg
 325 330 335
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<213> Escherichia coli

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 35 40 45
 Lys Ala Leu Leu Glu Tyr Asp Val Asp Cys His Cys Ile Pro Glu Leu
 50 55 60
 Thr Arg Glu Ile Thr Val Lys Asn Asp Phe Lys Ala Leu Phe Lys Leu
 65 70 75 80
 Tyr Lys Phe Ile Lys Lys Glu Lys Phe Asp Ile Val His Thr His Ser
 85 90 95
 Ser Lys Thr Gly Ile Leu Gly Arg Val Ala Ala Lys Leu Ala Arg Val
 100 105 110
 Gly Lys Val Ile His Thr Val His Gly Phe Ser Phe Pro Ala Ala Ser
 115 120 125
 Ser Lys Lys Ser Tyr Tyr Leu Tyr Phe Phe Met Glu Trp Ile Ala Lys
 130 135 140
 Phe Phe Thr Asp Lys Leu Ile Val Leu Asn Val Asp Asp Glu Tyr Ile
 145 150 155 160
 Ala Ile Asn Lys Leu Lys Phe Lys Arg Asp Lys Val Phe Leu Ile Pro
 165 170 175
 Asn Gly Val Asp Thr Asp Lys Phe Ser Pro Leu Glu Asn Lys Ile Tyr
 180 185 190
 Ser Ser Thr Leu Asn Leu Val Met Val Gly Arg Leu Ser Lys Gln Lys
 195 200 205
 Asp Pro Glu Thr Leu Leu Leu Ala Val Glu Lys Leu Leu Asn Glu Asn
 210 215 220
 Val Asn Val Lys Leu Thr Leu Val Gly Asp Gly Glu Leu Lys Glu Gln
 225 230 235 240
 Leu Glu Ser Arg Phe Lys Arg Gln Asp Gly Arg Ile Ile Phe His Gly
 245 250 255
 Trp Ser Asp Asn Ile Val Asn Ile Leu Lys Val Asn Asp Leu Phe Ile
 260 265 270
 Leu Pro Ser Leu Trp Glu Gly Met Pro Leu Ala Ile Leu Glu Ala Leu
 275 280 285
 Ser Cys Gly Leu Pro Cys Ile Val Thr Asn Ile Pro Gly Asn Asn Ser
 290 295 300

Leu Ile Glu Asp Gly Tyr Asn Gly Cys Leu Phe Glu Ile Arg Asp Cys
 305 310 315 320

Gln Leu Leu Ser Gln Lys Ile Met Ser Tyr Val Gly Lys Pro Glu Leu
 325 330 335

Ile Ala Gln Gln Ser Thr Asn Ala Arg Ser Phe Ile Leu Lys Asn Tyr
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<213> Escherichia coli

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 Gln Arg Cys Asp Leu Ile Ala Val Ile Asp Lys Gly Leu Leu Ala Glu
 20 25 30

tac gga acc cac gaa cag ctg tta tct gcg ggc ggc ctc tat acc cgc 143
 Tyr Gly Thr His Glu Gln Leu Leu Ser Ala Gly Gly Leu Tyr Thr Arg
 35 40 45

tta tgg cat gac agc gtc agc agt act gct ctc cat cgc cag cac aac 191
 Leu Trp His Asp Ser Val Ser Ser Thr Ala Leu His Arg Gln His Asn
 50 55 60

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 65 70

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75								80								
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Phe	Trp	Arg	Glu	Ala	Glu	Ser	Leu	Asn	Val	Pro	Leu	Val	Thr	Pro	Val	
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gaa	gga	gcg	gaa	gat	gag	cga	gaa	gtg	acc	ttt	ctg	tgg	cgc	gcc	cga	498
Glu	Gly	Ala	Glu	Asp	Glu	Arg	Glu	Val	Thr	Phe	Leu	Trp	Arg	Ala	Arg	
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cat	cct	ctg	cag	ggc	gtt	tat	ctg	cgt	ctg	aac	cgg	gtg	acg	gat	aaa	546
His	Pro	Leu	Gln	Gly	Val	Tyr	Leu	Arg	Leu	Asn	Arg	Val	Thr	Asp	Lys	
135				140				145								
gag	cac	gta	gaa	aaa	gga	atg	atg	agc	gcc	ctt	ccc	gaa	acg	gat	atc	594
Glu	His	Val	Glu	Lys	Gly	Met	Met	Ser	Ala	Leu	Pro	Glu	Thr	Asp	Ile	
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tgg	aca	ctg	aca	ctg	cgt	tta	ccc	gca	agt	tac	tgc	ggc	tcc	tat	tcg	642
Trp	Thr	Leu	Thr	Leu	Arg	Leu	Pro	Ala	Ser	Tyr	Cys	Gly	Ser	Tyr	Ser	
165		170				175										
ctg	ctg	gaa	atc	ccc	ccc	ggc	act	acg	gct	gag	acg	att	gca	ctg	tcc	690
Leu	Leu	Glu	Ile	Pro	Pro	Gly	Thr	Thr	Ala	Glu	Thr	Ile	Ala	Leu	Ser	
180		185				190				195						
gga	ggc	cgt	ttt	gcc	acc	ctt	gcc	gga	aag	gcc	gat	ccg	cta	aac	aaa	738
Gly	Gly	Arg	Phe	Ala	Thr	Leu	Ala	Gly	Lys	Ala	Asp	Pro	Leu	Asn	Lys	
200				205				210								
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Met	Pro	Glu	Ile	Asn	Val	Arg	Gly	Asn	Ala	Lys	Glu	Ser	Val	Leu	Thr	
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Leu	Asp	Lys	Ala	Pro	Ala	Leu	Ser	Glu	Trp	Asn	Gly	Gly	Phe	His	Thr	
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Ile	Pro	Asp	Val	Asp	Ile	Ser	Gln	Pro	Leu	Gly	Leu	Val	Val	Leu	Pro
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 Ser Glu Thr Asp Thr Ser Trp Val Ser Glu His Leu Leu Ser Ala Pro
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ccg cag ggc gta cgt atc agc ctg tgc gtg gga tcg ctg gaa ggt tcg 144
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Val Glu Ser His Cys Ala Ile Tyr Thr Gly Gly His Asp Tyr Ala Trp
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Thr Val Pro His Val Gln Gln Leu His Gln Arg Leu Ile Thr Ala Gly
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Arg His Tyr Arg Val Trp Thr Ala Val Pro Asn Thr Thr Ala Pro Ala
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 Lys Gly Val Asn Ala Val Phe Trp Asp Phe Pro Asn Leu Gly His Gly
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Pro Ser Lys Leu Thr Glu Asp Gln Lys Gln Thr Val Ser Thr Leu Ala	
100 105 110	
acg ctg tca gcg ggt atg gcc ggc ggc att gcc agt ggc gat gtg gct	385
Thr Leu Ser Ala Gly Met Ala Gly Gly Ile Ala Ser Gly Asp Val Ala	
115 120 125	
ggc gcg gct gct gga gct ggt gcc ggg aag aac gtt gtt gag aat aat	433
Gly Ala Ala Ala Gly Ala Gly Ala Gly Lys Asn Val Val Glu Asn Asn	
130 135 140	
gcg ctg agt ctg gtt gcc aga ggc tgt gcg gtc gca gca cct tgc agg	481
Ala Leu Ser Leu Val Ala Arg Gly Cys Ala Val Ala Ala Pro Cys Arg	
145 150 155 160	
act aaa gtt gca gag cag ttg cta gaa atc ggg gcg aaa gcg ggc atg	529
Thr Lys Val Ala Glu Gln Leu Leu Glu Ile Gly Ala Lys Ala Gly Met	
165 170 175	
gcc ggg ctt gcc ggg gcg gca gtc aag gat atg gcc gac agg atg acc	577
Ala Gly Leu Ala Gly Ala Ala Val Lys Asp Met Ala Asp Arg Met Thr	
180 185 190	
tcc gat gaa ctg gag cat ctg att acc ctg caa atg atg ggt aat gat	625
Ser Asp Glu Leu Glu His Leu Ile Thr Leu Gln Met Met Gly Asn Asp	
195 200 205	
gag atc act act aag tat ctc agt tcg ttg cat gat aag tac ggt tcc	673
Glu Ile Thr Thr Lys Tyr Leu Ser Ser Leu His Asp Lys Tyr Gly Ser	
210 215 220	
ggg gct gcc tcg aat ccg aat atc ggt aaa gat ctg acc gat gcg gaa	721
Gly Ala Ala Ser Asn Pro Asn Ile Gly Lys Asp Leu Thr Asp Ala Glu	
225 230 235 240	

aaa gta gaa ctg ggc ggt tcc ggc tca gga acc ggt aca cca cca cca	769
Lys Val Glu Leu Gly Gly Ser Gly Ser Gly Thr Gly Thr Pro Pro Pro	
245 250 255	
tcg gaa aat gat cct aag cag caa aat gaa aaa act gta gat aag ctt	817
Ser Glu Asn Asp Pro Lys Gln Gln Asn Glu Lys Thr Val Asp Lys Leu	
260 265 270	
aat cag aag caa gaa agt gcg att aag aag atc gat aac act ata aaa	865
Asn Gln Lys Gln Glu Ser Ala Ile Lys Lys Ile Asp Asn Thr Ile Lys	
275 280 285	
aat gct ctg aaa gat cat gat att att gga act ctc aag gat atg gat	913
Asn Ala Leu Lys Asp His Asp Ile Ile Gly Thr Leu Lys Asp Met Asp	
290 295 300	
ggg aag cca gtt cct aaa gag aat gga gga tat tgg gat cat atg cag	961
Gly Lys Pro Val Pro Lys Glu Asn Gly Gly Tyr Trp Asp His Met Gln	
305 310 315 320	
gaa atg caa aat acg ctc aga gga tta aga aat cat gcg gat acg ttg	1009
Glu Met Gln Asn Thr Leu Arg Gly Leu Arg Asn His Ala Asp Thr Leu	
325 330 335	
aaa aac gtc aac aat cct gaa gct cag gct gcg tat ggc aga gca aca	1057
Lys Asn Val Asn Asn Pro Glu Ala Gln Ala Ala Tyr Gly Arg Ala Thr	
340 345 350	
gat gct att aat aaa ata gaa tca gcc ttg aaa gga tat gga at atg	1104
Asp Ala Ile Asn Lys Ile Glu Ser Ala Leu Lys Gly Tyr Gly Met	
355 360 365	
att acc tta cgt aaa ttg att gga aac atc aat atg aca aaa gag cct	1152
Ile Thr Leu Arg Lys Leu Ile Gly Asn Ile Asn Met Thr Lys Glu Pro	
370 375 380	
gag caa caa tca ccg ctt gaa ctc tgg ttc gaa cgt atc ata gat gtg	1200
Glu Gln Gln Ser Pro Leu Glu Leu Trp Phe Glu Arg Ile Ile Asp Val	
385 390 395	
cct ctt gaa aag tta aca gtg gaa gat ctt tgc cgc gct atc cga caa	1248
Pro Leu Glu Lys Leu Thr Val Glu Asp Leu Cys Arg Ala Ile Arg Gln	
400 405 410 415	
aat tta tgt att gat cag ttg atg cca aga gtg ttg gaa gtt cta act	1296
Asn Leu Cys Ile Asp Gln Leu Met Pro Arg Val Leu Glu Val Leu Thr	
420 425 430	
aaa gag ccg tta gcg ggt gaa tat tac gat ggt gaa cta att gca gct	1344
Lys Glu Pro Leu Ala Gly Glu Tyr Tyr Asp Gly Glu Leu Ile Ala Ala	
435 440 445	

tta tca acg ata aaa gga gaa gat cta aaa gat cag aaa agt acc ttt 1392
 Leu Ser Thr Ile Lys Gly Glu Asp Leu Lys Asp Gln Lys Ser Thr Phe
 450 455 460

acc caa ata agg caa ctt ata aac cag cta gaa ccg tca gat att aac 1440
 Thr Gln Ile Arg Gln Leu Ile Asn Gln Leu Glu Pro Ser Asp Ile Asn
 465 470 475

gat gat tta aga aaa gat ata tta aaa atc aat cag ata att gta 1485
 Asp Asp Leu Arg Lys Asp Ile Leu Lys Ile Asn Gln Ile Ile Val
 480 485 490

taactaatcc cggccactga gccgagatct tctttgtgtg ccgggcatgt tcagcagctt 1545

gggggtgaaa gtcccctgtc cagcctg atg gtg gcg aag gcg ttc gcg tac gca 1599
 Met Val Ala Lys Ala Phe Ala Tyr Ala
 495 500

ctt aac cag tgg ccg gca ctg acg tac tat gcg aac gat ggc tgg gtg 1647
 Leu Asn Gln Trp Pro Ala Leu Thr Tyr Tyr Ala Asn Asp Gly Trp Val
 505 510 515

gaa atc gac aac aac atc gct gaa aat gcc ctg cgg gcg gtc agt ctg 1695
 Glu Ile Asp Asn Asn Ile Ala Glu Asn Ala Leu Arg Ala Val Ser Leu
 520 525 530 535

ggg cgt aaa aac ttc ctg ttc ttc ggc tct gac cat ggt ggt gag cgg 1743
 Gly Arg Lys Asn Phe Leu Phe Phe Gly Ser Asp His Gly Gly Glu Arg
 540 545 550

gga gcg cta ctg tac agc ctg atc ggg acg tgc aaa ctg aat gac gtg 1791
 Gly Ala Leu Leu Tyr Ser Leu Ile Gly Thr Cys Lys Leu Asn Asp Val
 555 560 565

gat cca gaa agc tac ctt cgc cat gtg ctt gcc gtc ata gca gac tgg 1839
 Asp Pro Glu Ser Tyr Leu Arg His Val Leu Ala Val Ile Ala Asp Trp
 570 575 580

ccg gtc aac cgg gtc agc gaa ctg ctt ccg tgg cgc ata gca ctg cca 1887
 Pro Val Asn Arg Val Ser Glu Leu Leu Pro Trp Arg Ile Ala Leu Pro
 585 590 595

gct gaa taacacatcc ccgtcaatac ggccctcgct gtacgcttag agaaa atg ctg 1944
 Ala Glu Met Leu
 600

atg tct gta cag aaa gaa aag aac gtc gca gag agt gtg gta tct gaa 1992
 Met Ser Val Gln Lys Glu Lys Asn Val Ala Glu Ser Val Val Ser Glu
 605 610 615

acg cat acc ggc gac agc gta tat gct tcc ctg ttt gaa aaa att aac 2040

Thr His Thr Gly Asp Ser Val Tyr Ala Ser Leu Phe Glu Lys Ile Asn	
620	625 630 635
ctg aat ccg gta tct gcc ctg agt gca ctg gat aac cct ttc cgg tca	2088
Leu Asn Pro Val Ser Ala Leu Ser Ala Leu Asp Asn Pro Phe Arg Ser	
640	645 650
gca gat aac gcg act ggc aga att acc tcc agc ata caa cct gcg gtg	2136
Ala Asp Asn Ala Thr Gly Arg Ile Thr Ser Ser Ile Gln Pro Ala Val	
655	660 665
cag tgc gca gct gct gca gca act gag ggt tct tgt ccc cgg caa tcc	2184
Gln Cys Ala Ala Ala Ala Ala Thr Glu Gly Ser Cys Pro Arg Gln Ser	
670	675 680
ccg tgt tca gga a atg gtg gat aac tgg cag aag agt gta agg agt cgt	2233
Pro Cys Ser Gly Met Val Asp Asn Trp Gln Lys Ser Val Arg Ser Arg	
685	690 695
gcg ctc ccg gaa gag gcg atg acg ggc tgg aac gaa ggc atg atc cgc	2281
Ala Leu Pro Glu Glu Ala Met Thr Gly Trp Asn Glu Gly Met Ile Arg	
700	705 710 715
tta cag cag ttg gct gag cgc ctg aac cgt cag gat gaa cag cgg gga	2329
Leu Gln Gln Leu Ala Glu Arg Leu Asn Arg Gln Asp Glu Gln Arg Gly	
720	725 730
aaa tac atg acg gtc agt gaa ctg aaa acg gag gtg ttt ggc atc atg	2377
Lys Tyr Met Thr Val Ser Glu Leu Lys Thr Glu Val Phe Gly Ile Met	
735	740 745
cag gct ttt aac cgg cat atc ccg gcg gaa gag cag tta cgt cgc tac	2425
Gln Ala Phe Asn Arg His Ile Pro Ala Glu Glu Gln Leu Arg Arg Tyr	
750	755 760
ggt gaa gtc cgt aac cag aat ggc agt gaa cag cag caa aaa cag gct	2473
Gly Glu Val Arg Asn Gln Asn Gly Ser Glu Gln Gln Gln Lys Gln Ala	
765	770 775
gaa atg gcg cta aat cag tta att aac cgt tat cag atg ata cgt gca	2521
Glu Met Ala Leu Asn Gln Leu Ile Asn Arg Tyr Gln Met Ile Arg Ala	
780	785 790 795
ggc aaa caa tagtggtagc cataatgcag gagcaaagcc tgaatcagga	2570
Gly Lys Gln	
agagttattc tgactgagtt tggttttctg gcgattcttg tg atg gtg gga tgt	2624
Met Val Gly Cys	
800	
gct tgg tta gct gaa cag gcc ttt tcc gac cat gcg ctt tca cca cac	2672

Ala Trp Leu Ala Glu Gln Ala Phe Ser Asp His Ala Leu Ser Pro His	
805 810 815	
agt gct tgg ccg tac agt gca tgc cgc gat gcc ggg ctg gcc gat acg	2720
Ser Ala Trp Pro Tyr Ser Ala Ser Arg Asp Ala Gly Leu Ala Asp Thr	
820 825 830	
ggc gcg ggc ggc tat ccc act tgt aaa cag cgg tgg gcc gac gac acc	2768
Gly Ala Gly Gly Tyr Pro Thr Cys Lys Gln Arg Trp Ala Asp Asp Thr	
835 840 845 850	
gtt ggg ctg aaa gcc cgt cta ctg caa ctt cct gcc cta gat atc tgg	2816
Val Gly Leu Lys Ala Arg Leu Leu Gln Leu Pro Ala Leu Asp Ile Trp	
855 860 865	
acg gcg ttt aaa aaa atc gac cag tgc cag gta gtg tat gaa gag gcc	2864
Thr Ala Phe Lys Lys Ile Asp Gln Ser Gln Val Val Tyr Glu Glu Ala	
870 875 880	
gtg ctg cgc tgc cgg gtc agt gaa cga aat atg cag gta tgc cag aat	2912
Val Leu Arg Ser Arg Val Ser Glu Arg Asn Met Gln Val Ser Gln Asn	
885 890 895	
ggg cgc gtt tat cca agc tat ggc ggt aac gtt gat ggc acc gtc gcc	2960
Gly Arg Val Tyr Pro Ser Tyr Gly Gly Asn Val Asp Gly Thr Val Ala	
900 905 910	
aat gcc gcc acc cgg ttg gca tcc ggc gct aga aat atc ctc ggc agc	3008
Asn Ala Ala Thr Arg Leu Ala Ser Gly Ala Arg Asn Ile Leu Gly Ser	
915 920 925 930	
ata gcg gca tgt acg gca ttc gac agc gtg cgt taggcactac cg atg gta	3059
Ile Ala Ala Cys Thr Ala Phe Asp Ser Val Arg Met Val	
935 940	
cag gcg cag ctg caa ata gcg ctg gtg atc tgt att ccg ctg ata acg	3107
Gln Ala Gln Leu Gln Ile Ala Leu Val Ile Cys Ile Pro Leu Ile Thr	
945 950 955	
ctc tgt tgc gcg tgg gat gtg aaa gta gtg atg acg ctg acg ttt gtg	3155
Leu Cys Ser Ala Trp Asp Val Lys Val Val Met Thr Leu Thr Phe Val	
960 965 970 975	
cag ttt gca cta ttt ttc ctc acc ttt tgg tgg gaa ctg gca cgg tgg	3203
Gln Phe Ala Leu Phe Phe Leu Thr Phe Trp Trp Glu Leu Ala Arg Trp	
980 985 990	
ctt gat agc tgg ctg ctg gat gtg ctc tac aac agc gat acc cac agt	3251
Leu Asp Ser Trp Leu Leu Asp Val Leu Tyr Asn Ser Asp Thr His Ser	
995 1000 1005	

agc tgg aat tta gcc ggg atc cag aat acg cag gat gac gtg att atc 3299
 Ser Trp Asn Leu Ala Gly Ile Gln Asn Thr Gln Asp Asp Val Ile Ile
 1010 1015 1020

aat ctg gtg atg agg ttg atg ttt ctg gtg ttg ccg aca ttc tgg ctg 3347
 Asn Leu Val Met Arg Leu Met Phe Leu Val Leu Pro Thr Phe Trp Leu
 1025 1030 1035

ggg gcg atg acg tgg gct gga gtg agg gtt ggc gtg gcg ctg aat gga 3395
 Gly Ala Met Thr Trp Ala Gly Val Arg Val Gly Val Ala Leu Asn Gly
 1040 1045 1050 1055

gcg ctg gcg gga tgattgggag gtgattcgcc aatctcactt tcctatacac 3447
 Ala Leu Ala Gly

atataaaatg ta atg aaa tat ctc ttt ttt gag aat ata cat tct ata ttt 3498
 Met Lys Tyr Leu Phe Phe Glu Asn Ile His Ser Ile Phe
 1060 1065 1070

tta aca ttc agt ctc ttc cga aca tct gtg tcg cct gat ttc cca atg 3546
 Leu Thr Phe Ser Leu Phe Arg Thr Ser Val Ser Pro Asp Phe Pro Met
 1075 1080 1085

att ttt gca ttg ccc tca atc att tta ggt caa ttt acg acc aac caa 3594
 Ile Phe Ala Leu Pro Ser Ile Ile Leu Gly Gln Phe Thr Thr Asn Gln
 1090 1095 1100

tta act aac ttt gtg ata tgt atg ggt aac acc gtt gaa cgt cgg ctg 3642
 Leu Thr Asn Phe Val Ile Cys Met Gly Asn Thr Val Glu Arg Arg Leu
 1105 1110 1115 1120

ggt gtt gtt cat aat ccc ttt aaa agg tct ggg gat ggc cat gac ctc 3690
 Gly Val Val His Asn Pro Phe Lys Arg Ser Gly Asp Gly His Asp Leu
 1125 1130 1135

agg gcg gta gcg tgaccaaagt tcatatccat accaattatt tttattttaa 3742
 Arg Ala Val Ala
 1140

atatcaactt attcgagttg ttttatttag ttcaaagaag gtatcaaa ttg ata gtt 3799
 Leu Ile Val

ata gat ttt ttt tgt ggc tgt ggt gga gcc agt gaa ggg cta cgt cag 3847
 Ile Asp Phe Phe Cys Gly Cys Gly Gly Ala Ser Glu Gly Leu Arg Gln
 1145 1150 1155

gct ggc ttt gat atc gag ctt gga tta gat att gac caa caa gca tca 3895
 Ala Gly Phe Asp Ile Glu Leu Gly Leu Asp Ile Asp Gln Gln Ala Ser
 1160 1165 1170 1175

gaa aca ttt aaa gct aat ttc cct gat gca aaa ttc atc caa gat gat 3943

Glu Thr Phe Lys Ala Asn Phe Pro Asp Ala Lys Phe Ile Gln Asp Asp	
1180 1185 1190	
att agg aaa atc gaa cct caa gat atc tcc gac atc att gat att aaa	3991
Ile Arg Lys Ile Glu Pro Gln Asp Ile Ser Asp Ile Ile Asp Ile Lys	
1195 1200 1205	
gct aaa cgg cct ttg tta ctg agt gca tgt gca cca tgt caa cca ttt	4039
Ala Lys Arg Pro Leu Leu Leu Ser Ala Cys Ala Pro Cys Gln Pro Phe	
1210 1215 1220	
tcg caa cag aat aaa aat aaa act agt gac gac tca agg aga aat cta	4087
Ser Gln Gln Asn Lys Asn Lys Thr Ser Asp Asp Ser Arg Arg Asn Leu	
1225 1230 1235	
cta aat gaa act cat cgt ttt att aga gaa ctt ctt cct gaa tat att	4135
Leu Asn Glu Thr His Arg Phe Ile Arg Glu Leu Leu Pro Glu Tyr Ile	
1240 1245 1250 1255	
atg ctt gaa aat gtt cct gga atg caa aaa att gat gaa gaa aaa gaa	4183
Met Leu Glu Asn Val Pro Gly Met Gln Lys Ile Asp Glu Glu Lys Glu	
1260 1265 1270	
ggc cca ttt cag gag ttt att aag cta ctt aaa gag tta gag tat aac	4231
Gly Pro Phe Gln Glu Phe Ile Lys Leu Leu Lys Glu Leu Glu Tyr Asn	
1275 1280 1285	
tat ata tct ttt ata gcc aat gct gag aac tat ggg att ccc caa aga	4279
Tyr Ile Ser Phe Ile Ala Asn Ala Glu Asn Tyr Gly Ile Pro Gln Arg	
1290 1295 1300	
aga aaa aga ctc gtg ctc tta gct agt cga gta ggt aaa gtt acc cta	4327
Arg Lys Arg Leu Val Leu Leu Ala Ser Arg Val Gly Lys Val Thr Leu	
1305 1310 1315	
cca gag ata acc cat ggt aaa aat aaa atc cca ttc aaa act gta cga	4375
Pro Glu Ile Thr His Gly Lys Asn Lys Ile Pro Phe Lys Thr Val Arg	
1320 1325 1330 1335	
gat tat atc cag gac ttc aca aag tta tgt tca gga gaa acc gac ccc	4423
Asp Tyr Ile Gln Asp Phe Thr Lys Leu Cys Ser Gly Glu Thr Asp Pro	
1340 1345 1350	
aaa gat cct tta cat agg gct gga aca ctg agc cct ctt aac cta aaa	4471
Lys Asp Pro Leu His Arg Ala Gly Thr Leu Ser Pro Leu Asn Leu Lys	
1355 1360 1365	
aga att atg cac act cca gaa gga ggg gat aga aga aat tgg cca gaa	4519
Arg Ile Met His Thr Pro Glu Gly Gly Asp Arg Arg Asn Trp Pro Glu	
1370 1375 1380	

gag tta gtt aat aaa tgc cat aaa aat tat gat ggc cac aca gat act 4567
 Glu Leu Val Asn Lys Cys His Lys Asn Tyr Asp Gly His Thr Asp Thr
 1385 1390 1395

tat gga aga atg agt tgg gat aag cct gcg cct aca ctt acg acg aaa 4615
 Tyr Gly Arg Met Ser Trp Asp Lys Pro Ala Pro Thr Leu Thr Thr Lys
 1400 1405 1410 1415

tgt aat agt tac tcc aat ggt cgt ttt ggg cat cct gac ccc act caa 4663
 Cys Asn Ser Tyr Ser Asn Gly Arg Phe Gly His Pro Asp Pro Thr Gln
 1420 1425 1430

cat aga gca att agc ata aga gaa gca tca aga tta caa aca ttt cct 4711
 His Arg Ala Ile Ser Ile Arg Glu Ala Ser Arg Leu Gln Thr Phe Pro
 1435 1440 1445

tta agc tat gtt ttt aaa ggt tcg ctg aat tca atg gca aag caa atc 4759
 Leu Ser Tyr Val Phe Lys Gly Ser Leu Asn Ser Met Ala Lys Gln Ile
 1450 1455 1460

ggc aat gct gta cct tgc gaa ctc gct aga cta ttt ggg cta cat ctc 4807
 Gly Asn Ala Val Pro Cys Glu Leu Ala Arg Leu Phe Gly Leu His Leu
 1465 1470 1475

ata gaa aat tgt act aat aag gat tca tagatatatg gctaaaataa 4854
 Ile Glu Asn Cys Thr Asn Lys Asp Ser
 1480 1485

gaacaaaggc tcgagctttg gac atg ctt ggc aga caa caa att gca ggt ata 4907
 Met Leu Gly Arg Gln Gln Ile Ala Gly Ile
 1490 1495

cct act gcc ttg agt gag tta ttt aaa aat gct cat gat gcc tat gct 4955
 Pro Thr Ala Leu Ser Glu Leu Phe Lys Asn Ala His Asp Ala Tyr Ala
 1500 1505 1510

gat aat gtc gaa gtt gat ttt ttt agg aaa gaa aat ctt ctt atc ttg 5003
 Asp Asn Val Glu Val Asp Phe Phe Arg Lys Glu Asn Leu Leu Ile Leu
 1515 1520 1525 1530

aga gat gat gga tta ggt atg aca acc gat gaa ttt gaa gag agg tgg 5051
 Arg Asp Asp Gly Leu Gly Met Thr Thr Asp Glu Phe Glu Glu Arg Trp
 1535 1540 1545

ttg act att gga acc tcc agc aaa tta atc gac gat gat gca att aat 5099
 Leu Thr Ile Gly Thr Ser Ser Lys Leu Ile Asp Asp Asp Ala Ile Asn
 1550 1555 1560

aaa cca gca gtg gat agt aat aaa gcc ttt cgc cct atc atg gga gag 5147
 Lys Pro Ala Val Asp Ser Asn Lys Ala Phe Arg Pro Ile Met Gly Glu
 1565 1570 1575

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Lys Gly Ile Gly Arg Leu Ser Ile Ala Ala Ile Gly Pro Gln Val Leu	
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gtt ctt act agg gcc aaa aga gac aat gag ctt aag cca tta gtt gct	5243
Val Leu Thr Arg Ala Lys Arg Asp Asn Glu Leu Lys Pro Leu Val Ala	
1595 1600 1605 1610	
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Ala Phe Val Asn Trp Ser Leu Phe Ala Ile Pro Ser Leu Asp Leu Asp	
1615 1620 1625	
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Asp Ile Glu Ile Pro Ile Arg Thr Ile Ile Asn Asp Glu Cys Phe Thr	
1630 1635 1640	
aaa aaa act ctt gat gag atg att gag caa gca aga aat aat tta gac	5387
Lys Lys Thr Leu Asp Glu Met Ile Glu Gln Ala Arg Asn Asn Leu Asp	
1645 1650 1655	
tct tta tca cac aaa ata tca aaa tca aaa gta tca caa ata aat aca	5435
Ser Leu Ser His Lys Ile Ser Lys Ser Lys Val Ser Gln Ile Asn Thr	
1660 1665 1670	
caa tta tca tct ttt gaa ttt gat cct att cta tgg gaa aaa aaa tta	5483
Gln Leu Ser Ser Phe Glu Phe Asp Pro Ile Leu Trp Glu Lys Lys Leu	
1675 1680 1685 1690	
ggg gga cta aga cta tct gga gat ggg cat gga act cac ttc ata ata	5531
Gly Gly Leu Arg Leu Ser Gly Asp Gly His Gly Thr His Phe Ile Ile	
1695 1700 1705	
atg cct acc gaa gaa ata tta ata gat gac att tcc acg agc gat agc	5579
Met Pro Thr Glu Glu Ile Leu Ile Asp Asp Ile Ser Thr Ser Asp Ser	
1710 1715 1720	
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Asn Lys Thr Ser Glu Gln Ser Ser Arg Leu Glu Lys Ala Leu Leu Gly	
1725 1730 1735	
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Phe Thr Asn Thr Met Tyr Ser Asp Ser Asn Pro Pro Ile Ile Ala Arg	
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Phe Arg Asp Tyr Leu Glu Asp Gly Glu Cys Ile Asp Arg Ile Ser Glu	
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Ser Ile Phe Phe Thr Pro Gln Glu Phe Asn Leu Ala Asp His His Ile	
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tat ggt gaa gag cca att cat cat gtc gtg act tgg aaa aat aat aat Tyr Gly Glu Glu Pro Ile His His Val Val Thr Trp Lys Asn Asn Asn 1805 1810 1815	5867
caa tta acc caa tgc ggt cca ttt aaa ata aaa tta gcg tat att cat Gln Leu Thr Gln Cys Gly Pro Phe Lys Ile Lys Leu Ala Tyr Ile His 1820 1825 1830	5915
ggt cgg ctt cgt gat tca cgc tta ccc atg gag ttg tgg gcc cct ctg Gly Arg Leu Arg Asp Ser Arg Leu Pro Met Glu Leu Trp Ala Pro Leu 1835 1840 1845 1850	5963
aag gag aaa aca gat aga tat ggt ggt tta tat atc tat cga gat gga Lys Glu Lys Thr Asp Arg Tyr Gly Gly Leu Tyr Ile Tyr Arg Asp Gly 1855 1860 1865	6011
tta aga att ttg ccc tat gga gat tca gat acg gat ttt cta aaa ata Leu Arg Ile Leu Pro Tyr Gly Asp Ser Asp Thr Asp Phe Leu Lys Ile 1870 1875 1880	6059
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gtt gaa aaa gct ggg cga gaa gga ttc att gaa aat aag cca tat aaa Val Glu Lys Ala Gly Arg Glu Gly Phe Ile Glu Asn Lys Pro Tyr Lys 1915 1920 1925 1930	6203
cag ttt aaa gaa atg ctt gaa aat ttc ttc atc gaa atc gca aga gat Gln Phe Lys Glu Met Leu Glu Asn Phe Phe Ile Glu Ile Ala Arg Asp 1935 1940 1945	6251
ttc ttt aag gac gat ggc gat atg tct gaa tta ttt gtt gag aca aag Phe Phe Lys Asp Asp Gly Asp Met Ser Glu Leu Phe Val Glu Thr Lys 1950 1955 1960	6299
caa cgt aga aat gaa gaa cat gat ttg tta tct aaa aga tct aaa caa Gln Arg Arg Asn Glu Glu His Asp Leu Leu Ser Lys Arg Ser Lys Gln 1965 1970 1975	6347
act aaa gct aaa aaa gat aga tta aag aaa gat ctg tat gat ttt ttt Thr Lys Ala Lys Lys Asp Arg Leu Lys Lys Asp Leu Tyr Asp Phe Phe 1980 1985 1990	6395

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2205 2210 2215	
tca tcg gct caa gta act gaa gca atc gaa act gaa ctt gaa cat tta	7115
Ser Ser Ala Gln Val Thr Glu Ala Ile Glu Thr Glu Leu Glu His Leu	
2220 2225 2230	
cga gac caa caa gca aat aac gca gag tta ata cta ctt ggc atg gct	7163
Arg Asp Gln Gln Ala Asn Asn Ala Glu Leu Ile Leu Leu Gly Met Ala	
2235 2240 2245 2250	
ctt tct gta gta cat cat gaa ttt aat ggt aat att agg gca att aga	7211
Leu Ser Val Val His His Glu Phe Asn Gly Asn Ile Arg Ala Ile Arg	
2255 2260 2265	
agt gcg cta agg gaa tta aaa gca tgg gct gac aga aat cct aag ctt	7259
Ser Ala Leu Arg Glu Leu Lys Ala Trp Ala Asp Arg Asn Pro Lys Leu	
2270 2275 2280	
gat att ata tac caa aaa atc aga act agt ttt gat cac tta gat ggt	7307
Asp Ile Ile Tyr Gln Lys Ile Arg Thr Ser Phe Asp His Leu Asp Gly	
2285 2290 2295	
tat tta aaa acc ttt aca cca ttg aca aga cgt tta agt cgc tct aaa	7355
Tyr Leu Lys Thr Phe Thr Pro Leu Thr Arg Arg Leu Ser Arg Ser Lys	
2300 2305 2310	
acc aat ata act gga act gcc att tta gaa ttt atc aga gat gta ttc	7403
Thr Asn Ile Thr Gly Thr Ala Ile Leu Glu Phe Ile Arg Asp Val Phe	
2315 2320 2325 2330	
gat gat cgt ctt gag aaa gaa gga att gaa tta ttc act acc tca aag	7451
Asp Asp Arg Leu Glu Lys Glu Gly Ile Glu Leu Phe Thr Thr Ser Lys	
2335 2340 2345	
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Phe Val Asn Gln Glu Ile Val Thr Tyr Thr Ser Thr Ile Tyr Pro Val	
2350 2355 2360	
ttt ata aat cta att gat aac gca ata tac tgg ctt ggg aaa aca act	7547
Phe Ile Asn Leu Ile Asp Asn Ala Ile Tyr Trp Leu Gly Lys Thr Thr	
2365 2370 2375	
gga gaa aaa aga ctt ata ctt gat gct act gaa aca gga ttt gtt att	7595
Gly Glu Lys Arg Leu Ile Leu Asp Ala Thr Glu Thr Gly Phe Val Ile	
2380 2385 2390	
ggg gat act ggt ccc ggt gtt tca act aga gat cga gat ata ata ttt	7643
Gly Asp Thr Gly Pro Gly Val Ser Thr Arg Asp Arg Asp Ile Ile Phe	
2395 2400 2405 2410	

gat atg gga ttt aca cga aaa aca gga ggg cgt gga atg gga tta ttc Asp Met Gly Phe Thr Arg Lys Thr Gly Gly Arg Gly Met Gly Leu Phe 2415 2420 2425	7691
att tcc aaa gag tgt tta tct cga gat gga ttt act ata aga ttg gat Ile Ser Lys Glu Cys Leu Ser Arg Asp Gly Phe Thr Ile Arg Leu Asp 2430 2435 2440	7739
gat tac act cct gaa cag ggt gct ttc ttt att att gag cca tca gaa Asp Tyr Thr Pro Glu Gln Gly Ala Phe Phe Ile Ile Glu Pro Ser Glu 2445 2450 2455	7787
gaa aca agt gaa tag cggatataaa taa atg aca agc tct act gat ttt Glu Thr Ser Glu Met Thr Ser Ser Thr Asp Phe 2460 2465 2470	7836
cat aaa ctt tct gaa gac tgc gtt cgc cgt ttt tta cat tct gta gtt His Lys Leu Ser Glu Asp Cys Val Arg Arg Phe Leu His Ser Val Val 2475 2480 2485	7884
gct gta gat gac aat atg tct ttt gga gct ggt agt gat act ttc cct Ala Val Asp Asp Asn Met Ser Phe Gly Ala Gly Ser Asp Thr Phe Pro 2490 2495 2500	7932
aca gac gaa gat att aat gct tta gtt gat ccc gac gat gat cct aca Thr Asp Glu Asp Ile Asn Ala Leu Val Asp Pro Asp Asp Asp Pro Thr 2505 2510 2515	7980
cca ata ata aca gca tca gca tcc cca agg ata gaa tca act aaa tca Pro Ile Ile Thr Ala Ser Ala Ser Pro Arg Ile Glu Ser Thr Lys Ser 2520 2525 2530	8028
aaa gca aag gta aaa aac cat cct ttt gat tac caa gct cta gca gaa Lys Ala Lys Val Lys Asn His Pro Phe Asp Tyr Gln Ala Leu Ala Glu 2535 2540 2545 2550	8076
gct ttc gcc aaa gat ggt att gct tgt tgc gga tta tta gct aag agt Ala Phe Ala Lys Asp Gly Ile Ala Cys Cys Gly Leu Leu Ala Lys Ser 2555 2560 2565	8124
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gat ata aca ata ctt gac tgg gat atg caa agc gat agt ggg caa ttt Asp Ile Thr Ile Leu Asp Trp Asp Met Gln Ser Asp Ser Gly Gln Phe 2585 2590 2595	8220
gct att gaa ata ata aaa tcg ata atc gtt tca gat ata aat tct gga Ala Ile Glu Ile Ile Lys Ser Ile Ile Val Ser Asp Ile Asn Ser Gly 2600 2605 2610	8268

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gaa gaa gat aaa aag tta atg caa tta tgc tct ctg gaa atc acg cgc Glu Glu Asp Lys Lys Leu Met Gln Leu Cys Ser Leu Glu Ile Thr Arg 2840 2845 2850	8988
agg agt tta aga tat cat tct cat ata gat aat gtg tcc tta aaa caa Arg Ser Leu Arg Tyr His Ser His Ile Asp Asn Val Ser Leu Lys Gln 2855 2860 2865 2870	9036
gga act tta ctt tta gat gca tat aat ttt gtc tat cta tgc ata caa Gly Thr Leu Leu Leu Asp Ala Tyr Asn Phe Val Tyr Leu Cys Ile Gln 2875 2880 2885	9084
cca tta tgt gat agc gtc aga ttg cat gaa aaa gcc gat ttt tta ttc Pro Leu Cys Asp Ser Val Arg Leu His Glu Lys Ala Asp Phe Leu Phe 2890 2895 2900	9132
ctc agg gga aca ctg gac gat aat aat tac aat ttg tta atc gaa gat Leu Arg Gly Thr Leu Asp Asp Asn Asn Tyr Asn Leu Leu Ile Glu Asp 2905 2910 2915	9180
gaa tat ggc ggt ttt tat aaa att aaa atg ccg gca aaa gct tct aat Glu Tyr Gly Gly Phe Tyr Lys Ile Lys Met Pro Ala Lys Ala Ser Asn 2920 2925 2930	9228
att att tca ttt tca ttt gga gtc gaa aat gga aac ggt gtc atc ata Ile Ile Ser Phe Ser Phe Gly Val Glu Asn Gly Asn Gly Val Ile Ile 2935 2940 2945 2950	9276
ggg aaa aag aac aat cta gtt aat act gac tat atc tca ttc gtt cct Gly Lys Lys Asn Asn Leu Val Asn Thr Asp Tyr Ile Ser Phe Val Pro 2955 2960 2965	9324
tta ctc gtt gaa aaa ata tct act cca aaa gta ttg aaa tgg atc ggg Leu Leu Val Glu Lys Ile Ser Thr Pro Lys Val Leu Lys Trp Ile Gly 2970 2975 2980	9372
gaa ata aaa aca acg tac gcg caa aaa ata aca act gat att gtt gct Glu Ile Lys Thr Thr Tyr Ala Gln Lys Ile Thr Thr Asp Ile Val Ala 2985 2990 2995	9420
aat ctg tca aga ata ggt tta gat caa cat gag tgg tta cga ata aaa Asn Leu Ser Arg Ile Gly Leu Asp Gln His Glu Trp Leu Arg Ile Lys 3000 3005 3010	9468
tca aaa gat ata taaatgatta tatatgccgt cgttttataa aaactggcgg Ser Lys Asp Ile 3015	9520

catgtatatc tagttagtcc atcatagaag tcaagaaatt tagtttgccc tatatcttat 9580
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aatttatattg ttctatttta cacttactgc aaatagcatc cagtttatca tatagtgtcg 9820
catcaattgg cgcag atg tca tca cgc caa atc ctt gag cat tat aat gct 9871
Met Ser Ser Arg Gln Ile Leu Glu His Tyr Asn Ala
3020 3025 3030
cta aca tat ccc cta cat caa tca atc ttg ttg cag ata atg act tcg 9919
Leu Thr Tyr Pro Leu His Gln Ser Ile Leu Leu Gln Ile Met Thr Ser
3035 3040 3045
aat ttg tta tca gtt tgc act gga aaa tcc att tac gag gat atc tcc 9967
Asn Leu Leu Ser Val Cys Thr Gly Lys Ser Ile Tyr Glu Asp Ile Ser
3050 3055 3060
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Gly Ser Ser Trp Asn Ile Ile His Phe Asn Ile Pro Leu Pro Ile Ser
3065 3070 3075
aga gcg aga ctt tcc ata ttt tct tat tgt gtc aga att aaa cct tgg 10063
Arg Ala Arg Leu Ser Ile Phe Ser Tyr Cys Val Arg Ile Lys Pro Trp
3080 3085 3090
atg agt atg gat tac atg taaccggctc atttaaaccg tctggtctgt 10111
Met Ser Met Asp Tyr Met
3095 3100
ttcctccggt ttacaaaaa ta atg tcc atc att ttt aat gga cac tat cgt 10163
Met Ser Ile Ile Phe Asn Gly His Tyr Arg
3105 3110
atg aaa cac cgg act tgg atc act gaa gct tta cgt ctt cac ttt gaa 10211
Met Lys His Arg Thr Trp Ile Thr Glu Ala Leu Arg Leu His Phe Glu
3115 3120 3125
gaa cat tta ccc cag gtt gtg gtc ggg cgt cgc ctg ggc gta cca aaa 10259
Glu His Leu Pro Gln Val Val Val Gly Arg Arg Leu Gly Val Pro Lys
3130 3135 3140
tca aca gct tgt ggt atg ttc gtg cgc ttt cgc aaa gct ggc ttt tca 10307
Ser Thr Ala Cys Gly Met Phe Val Arg Phe Arg Lys Ala Gly Phe Ser
3145 3150 3155
tgg cct ctg ccc gca ggt atg tcg gag cgg gag ctt gat ggc cgt ctt 10355

Trp Pro Leu Pro Ala Gly Met Ser Glu Arg Glu Leu Asp Gly Arg Leu
 3160 3165 3170
 tac ggg agt acc tcc aca gta cct gtc gta ctt tgt agt gga tcg gta 10403
 Tyr Gly Ser Thr Ser Thr Val Pro Val Val Leu Cys Ser Gly Ser Val
 3175 3180 3185 3190
 att cag gac acc tcg aaa tcc tgt taatgttaaa acagtgaataa tgaggtgatg 10457
 Ile Gln Asp Thr Ser Lys Ser Cys
 3195
 c atg atc aaa act cgt cgg act aaa cgt acc ttt tcc ccg gag ttc aag 10506
 Met Ile Lys Thr Arg Arg Thr Lys Arg Thr Phe Ser Pro Glu Phe Lys
 3200 3205 3210
 ctt gaa gct ttc gag cag gtg gtg gtt aaa tac cag cgt gat gtc aga 10554
 Leu Glu Ala Phe Glu Gln Val Val Val Lys Tyr Gln Arg Asp Val Arg
 3215 3220 3225 3230
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 Glu Val Ala Gln Ala Leu Glu Leu Asn Pro Asp His Leu Arg Lys Trp
 3235 3240 3245
 ata cgg ttg tat aag cag gaa ctt cag ggt att gag cca gct ggt aat 10650
 Ile Arg Leu Tyr Lys Gln Glu Leu Gln Gly Ile Glu Pro Ala Gly Asn
 3250 3255 3260
 gct att acc cct gaa caa cgc gaa att cag cag ctt aaa gcg cag ata 10698
 Ala Ile Thr Pro Glu Gln Arg Glu Ile Gln Gln Leu Lys Ala Gln Ile
 3265 3270 3275
 aag cgc gtt gag atg gaa aaa gaa ata cta aag cag gct gcc gtg ctg 10746
 Lys Arg Val Glu Met Glu Lys Glu Ile Leu Lys Gln Ala Ala Val Leu
 3280 3285 3290
 atg agc gaa atc ccc ggg aag ctg tcg cgc taatcacaca gctgaaagca 10796
 Met Ser Glu Ile Pro Gly Lys Leu Ser Arg
 3295 3300
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ttttattcg

11165

<210> 35

<211> 366

<212> PRT

<213> Escherichia coli

<400> 35

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Leu Val Gly Gly Asn Met Ala Gly Ala Leu Ala Gly Ala Ser Ala Pro
 20 25 30

Glu Leu Ala Asn Ile Ile Gly His His Ala Gly Ile Asp Asp Asn Thr
 35 40 45

Ala Ala Lys Ala Ile Ala His Ala Ile Leu Gly Gly Val Thr Ala Ala
 50 55 60

Leu Gln Gly Asn Ser Ala Ala Ala Gly Ala Ile Gly Ala Gly Thr Gly
 65 70 75 80

Glu Val Ile Ala Ser Ala Ile Ala Lys Ser Leu Tyr Pro Gly Val Asp
 85 90 95

Pro Ser Lys Leu Thr Glu Asp Gln Lys Gln Thr Val Ser Thr Leu Ala
 100 105 110

Thr Leu Ser Ala Gly Met Ala Gly Gly Ile Ala Ser Gly Asp Val Ala
 115 120 125

Gly Ala Ala Ala Gly Ala Gly Ala Gly Lys Asn Val Val Glu Asn Asn
 130 135 140

Ala Leu Ser Leu Val Ala Arg Gly Cys Ala Val Ala Ala Pro Cys Arg
 145 150 155 160

Thr Lys Val Ala Glu Gln Leu Leu Glu Ile Gly Ala Lys Ala Gly Met
 165 170 175

Ala Gly Leu Ala Gly Ala Ala Val Lys Asp Met Ala Asp Arg Met Thr
 180 185 190

Ser Asp Glu Leu Glu His Leu Ile Thr Leu Gln Met Met Gly Asn Asp
 195 200 205

Glu Ile Thr Thr Lys Tyr Leu Ser Ser Leu His Asp Lys Tyr Gly Ser
 210 215 220

Gly Ala Ala Ser Asn Pro Asn Ile Gly Lys Asp Leu Thr Asp Ala Glu
 225 230 235 240
 Lys Val Glu Leu Gly Gly Ser Gly Ser Gly Thr Gly Thr Pro Pro Pro
 245 250 255
 Ser Glu Asn Asp Pro Lys Gln Gln Asn Glu Lys Thr Val Asp Lys Leu
 260 265 270
 Asn Gln Lys Gln Glu Ser Ala Ile Lys Lys Ile Asp Asn Thr Ile Lys
 275 280 285
 Asn Ala Leu Lys Asp His Asp Ile Ile Gly Thr Leu Lys Asp Met Asp
 290 295 300
 Gly Lys Pro Val Pro Lys Glu Asn Gly Gly Tyr Trp Asp His Met Gln
 305 310 315 320
 Glu Met Gln Asn Thr Leu Arg Gly Leu Arg Asn His Ala Asp Thr Leu
 325 330 335
 Lys Asn Val Asn Asn Pro Glu Ala Gln Ala Ala Tyr Gly Arg Ala Thr
 340 345 350
 Asp Ala Ile Asn Lys Ile Glu Ser Ala Leu Lys Gly Tyr Gly
 355 360 365

<210> 36
 <211> 128
 <212> PRT
 <213> Escherichia coli

<400> 36
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 Pro Glu Gln Gln Ser Pro Leu Glu Leu Trp Phe Glu Arg Ile Ile Asp
 20 25 30
 Val Pro Leu Glu Lys Leu Thr Val Glu Asp Leu Cys Arg Ala Ile Arg
 35 40 45
 Gln Asn Leu Cys Ile Asp Gln Leu Met Pro Arg Val Leu Glu Val Leu
 50 55 60
 Thr Lys Glu Pro Leu Ala Gly Glu Tyr Tyr Asp Gly Glu Leu Ile Ala
 65 70 75 80
 Ala Leu Ser Thr Ile Lys Gly Glu Asp Leu Lys Asp Gln Lys Ser Thr
 85 90 95

Phe Thr Gln Ile Arg Gln Leu Ile Asn Gln Leu Glu Pro Ser Asp Ile
 100 105 110

Asn Asp Asp Leu Arg Lys Asp Ile Leu Lys Ile Asn Gln Ile Ile Val
 115 120 125

<210> 37

<211> 107

<212> PRT

<213> Escherichia coli

<400> 37

Met Val Ala Lys Ala Phe Ala Tyr Ala Leu Asn Gln Trp Pro Ala Leu
 1 5 10 15

Thr Tyr Tyr Ala Asn Asp Gly Trp Val Glu Ile Asp Asn Asn Ile Ala
 20 25 30

Glu Asn Ala Leu Arg Ala Val Ser Leu Gly Arg Lys Asn Phe Leu Phe
 35 40 45

Phe Gly Ser Asp His Gly Gly Glu Arg Gly Ala Leu Leu Tyr Ser Leu
 50 55 60

Ile Gly Thr Cys Lys Leu Asn Asp Val Asp Pro Glu Ser Tyr Leu Arg
 65 70 75 80

His Val Leu Ala Val Ile Ala Asp Trp Pro Val Asn Arg Val Ser Glu
 85 90 95

Leu Leu Pro Trp Arg Ile Ala Leu Pro Ala Glu
 100 105

<210> 38

<211> 86

<212> PRT

<213> Escherichia coli

<400> 38

Met Leu Met Ser Val Gln Lys Glu Lys Asn Val Ala Glu Ser Val Val
 1 5 10 15

Ser Glu Thr His Thr Gly Asp Ser Val Tyr Ala Ser Leu Phe Glu Lys
 20 25 30

Ile Asn Leu Asn Pro Val Ser Ala Leu Ser Ala Leu Asp Asn Pro Phe
 35 40 45

Arg Ser Ala Asp Asn Ala Thr Gly Arg Ile Thr Ser Ser Ile Gln Pro

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<400> 39
Met Val Asp Asn Trp Gln Lys Ser Val Arg Ser Arg Ala Leu Pro Glu
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Glu Ala Met Thr Gly Trp Asn Glu Gly Met Ile Arg Leu Gln Gln Leu
      20                      25                      30
Ala Glu Arg Leu Asn Arg Gln Asp Glu Gln Arg Gly Lys Tyr Met Thr
      35                      40                      45
Val Ser Glu Leu Lys Thr Glu Val Phe Gly Ile Met Gln Ala Phe Asn
      50                      55                      60
Arg His Ile Pro Ala Glu Glu Gln Leu Arg Arg Tyr Gly Glu Val Arg
  65                      70                      75                      80
Asn Gln Asn Gly Ser Glu Gln Gln Gln Lys Gln Ala Glu Met Ala Leu
      85                      90                      95
Asn Gln Leu Ile Asn Arg Tyr Gln Met Ile Arg Ala Gly Lys Gln
      100                      105                      110

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<400> 40
Met Val Gly Cys Ala Trp Leu Ala Glu Gln Ala Phe Ser Asp His Ala
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          20             25             30
Leu Ala Asp Thr Gly Ala Gly Gly Tyr Pro Thr Cys Lys Gln Arg Trp
          35             40             45

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Ala Asp Asp Thr Val Gly Leu Lys Ala Arg Leu Leu Gln Leu Pro Ala
 50 55 60

Leu Asp Ile Trp Thr Ala Phe Lys Lys Ile Asp Gln Ser Gln Val Val
 65 70 75 80

Tyr Glu Glu Ala Val Leu Arg Ser Arg Val Ser Glu Arg Asn Met Gln
 85 90 95

Val Ser Gln Asn Gly Arg Val Tyr Pro Ser Tyr Gly Gly Asn Val Asp
 100 105 110

Gly Thr Val Ala Asn Ala Ala Thr Arg Leu Ala Ser Gly Ala Arg Asn
 115 120 125

Ile Leu Gly Ser Ile Ala Ala Cys Thr Ala Phe Asp Ser Val Arg
 130 135 140

<210> 41

<211> 118

<212> PRT

<213> Escherichia coli

<400> 41

Met Val Gln Ala Gln Leu Gln Ile Ala Leu Val Ile Cys Ile Pro Leu
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Ile Thr Leu Cys Ser Ala Trp Asp Val Lys Val Val Met Thr Leu Thr
 20 25 30

Phe Val Gln Phe Ala Leu Phe Phe Leu Thr Phe Trp Trp Glu Leu Ala
 35 40 45

Arg Trp Leu Asp Ser Trp Leu Leu Asp Val Leu Tyr Asn Ser Asp Thr
 50 55 60

His Ser Ser Trp Asn Leu Ala Gly Ile Gln Asn Thr Gln Asp Asp Val
 65 70 75 80

Ile Ile Asn Leu Val Met Arg Leu Met Phe Leu Val Leu Pro Thr Phe
 85 90 95

Trp Leu Gly Ala Met Thr Trp Ala Gly Val Arg Val Gly Val Ala Leu
 100 105 110

Asn Gly Ala Leu Ala Gly
 115

<210> 42

<211> 81
 <212> PRT
 <213> Escherichia coli

<400> 42
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 20 25 30
 Leu Pro Ser Ile Ile Leu Gly Gln Phe Thr Thr Asn Gln Leu Thr Asn
 35 40 45
 Phe Val Ile Cys Met Gly Asn Thr Val Glu Arg Arg Leu Gly Val Val
 50 55 60
 His Asn Pro Phe Lys Arg Ser Gly Asp Gly His Asp Leu Arg Ala Val
 65 70 75 80
 Ala

<210> 43
 <211> 348
 <212> PRT
 <213> Escherichia coli

<400> 43
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 Leu Arg Gln Ala Gly Phe Asp Ile Glu Leu Gly Leu Asp Ile Asp Gln
 20 25 30
 Gln Ala Ser Glu Thr Phe Lys Ala Asn Phe Pro Asp Ala Lys Phe Ile
 35 40 45
 Gln Asp Asp Ile Arg Lys Ile Glu Pro Gln Asp Ile Ser Asp Ile Ile
 50 55 60
 Asp Ile Lys Ala Lys Arg Pro Leu Leu Leu Ser Ala Cys Ala Pro Cys
 65 70 75 80
 Gln Pro Phe Ser Gln Gln Asn Lys Asn Lys Thr Ser Asp Asp Ser Arg
 85 90 95
 Arg Asn Leu Leu Asn Glu Thr His Arg Phe Ile Arg Glu Leu Leu Pro
 100 105 110
 Glu Tyr Ile Met Leu Glu Asn Val Pro Gly Met Gln Lys Ile Asp Glu

115					120					125						
Glu	Lys	Glu	Gly	Pro	Phe	Gln	Glu	Phe	Ile	Lys	Leu	Leu	Lys	Glu	Leu	
130					135					140						
Glu	Tyr	Asn	Tyr	Ile	Ser	Phe	Ile	Ala	Asn	Ala	Glu	Asn	Tyr	Gly	Ile	
145					150					155					160	
Pro	Gln	Arg	Arg	Lys	Arg	Leu	Val	Leu	Leu	Ala	Ser	Arg	Val	Gly	Lys	
165					170					175						
Val	Thr	Leu	Pro	Glu	Ile	Thr	His	Gly	Lys	Asn	Lys	Ile	Pro	Phe	Lys	
180					185					190						
Thr	Val	Arg	Asp	Tyr	Ile	Gln	Asp	Phe	Thr	Lys	Leu	Cys	Ser	Gly	Glu	
195					200					205						
Thr	Asp	Pro	Lys	Asp	Pro	Leu	His	Arg	Ala	Gly	Thr	Leu	Ser	Pro	Leu	
210					215					220						
Asn	Leu	Lys	Arg	Ile	Met	His	Thr	Pro	Glu	Gly	Gly	Asp	Arg	Arg	Asn	
225					230					235					240	
Trp	Pro	Glu	Glu	Leu	Val	Asn	Lys	Cys	His	Lys	Asn	Tyr	Asp	Gly	His	
245					250					255						
Thr	Asp	Thr	Tyr	Gly	Arg	Met	Ser	Trp	Asp	Lys	Pro	Ala	Pro	Thr	Leu	
260					265					270						
Thr	Thr	Lys	Cys	Asn	Ser	Tyr	Ser	Asn	Gly	Arg	Phe	Gly	His	Pro	Asp	
275					280					285						
Pro	Thr	Gln	His	Arg	Ala	Ile	Ser	Ile	Arg	Glu	Ala	Ser	Arg	Leu	Gln	
290					295					300						
Thr	Phe	Pro	Leu	Ser	Tyr	Val	Phe	Lys	Gly	Ser	Leu	Asn	Ser	Met	Ala	
305					310					315					320	
Lys	Gln	Ile	Gly	Asn	Ala	Val	Pro	Cys	Glu	Leu	Ala	Arg	Leu	Phe	Gly	
325					330					335						
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340					345											

<210> 44

<211> 974

<212> PRT

<213> Escherichia coli

<400> 44

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 Phe Phe Arg Lys Glu Asn Leu Leu Ile Leu Arg Asp Asp Gly Leu Gly
 35 40 45
 Met Thr Thr Asp Glu Phe Glu Glu Arg Trp Leu Thr Ile Gly Thr Ser
 50 55 60
 Ser Lys Leu Ile Asp Asp Asp Ala Ile Asn Lys Pro Ala Val Asp Ser
 65 70 75 80
 Asn Lys Ala Phe Arg Pro Ile Met Gly Glu Lys Gly Ile Gly Arg Leu
 85 90 95
 Ser Ile Ala Ala Ile Gly Pro Gln Val Leu Val Leu Thr Arg Ala Lys
 100 105 110
 Arg Asp Asn Glu Leu Lys Pro Leu Val Ala Ala Phe Val Asn Trp Ser
 115 120 125
 Leu Phe Ala Ile Pro Ser Leu Asp Leu Asp Asp Ile Glu Ile Pro Ile
 130 135 140
 Arg Thr Ile Ile Asn Asp Glu Cys Phe Thr Lys Lys Thr Leu Asp Glu
 145 150 155 160
 Met Ile Glu Gln Ala Arg Asn Asn Leu Asp Ser Leu Ser His Lys Ile
 165 170 175
 Ser Lys Ser Lys Val Ser Gln Ile Asn Thr Gln Leu Ser Ser Phe Glu
 180 185 190
 Phe Asp Pro Ile Leu Trp Glu Lys Lys Leu Gly Gly Leu Arg Leu Ser
 195 200 205
 Gly Asp Gly His Gly Thr His Phe Ile Ile Met Pro Thr Glu Glu Ile
 210 215 220
 Leu Ile Asp Asp Ile Ser Thr Ser Asp Ser Asn Lys Thr Ser Glu Gln
 225 230 235 240
 Ser Ser Arg Leu Glu Lys Ala Leu Leu Gly Phe Thr Asn Thr Met Tyr
 245 250 255
 Ser Asp Ser Asn Pro Pro Ile Ile Ala Arg Phe Arg Asp Tyr Leu Glu
 260 265 270

Asp Gly Glu Cys Ile Asp Arg Ile Ser Glu Ser Ile Phe Phe Thr Pro
 275 280 285
 Gln Glu Phe Asn Leu Ala Asp His His Ile Glu Gly Trp Phe Asn Glu
 290 295 300
 Phe Gly Gln Phe Ser Gly Thr Val Ser Val Tyr Gly Glu Glu Pro Ile
 305 310 315 320
 His His Val Val Thr Trp Lys Asn Asn Asn Gln Leu Thr Gln Cys Gly
 325 330 335
 Pro Phe Lys Ile Lys Leu Ala Tyr Ile His Gly Arg Leu Arg Asp Ser
 340 345 350
 Arg Leu Pro Met Glu Leu Trp Ala Pro Leu Lys Glu Lys Thr Asp Arg
 355 360 365
 Tyr Gly Gly Leu Tyr Ile Tyr Arg Asp Gly Leu Arg Ile Leu Pro Tyr
 370 375 380
 Gly Asp Ser Asp Thr Asp Phe Leu Lys Ile Glu Lys Arg Arg Thr Leu
 385 390 395 400
 Ser Ala Ser Glu Tyr Phe Phe Ser Tyr Arg Arg Leu Phe Gly Ala Ile
 405 410 415
 Glu Leu Thr Lys Glu Asn Asn Ala Ser Leu Val Glu Lys Ala Gly Arg
 420 425 430
 Glu Gly Phe Ile Glu Asn Lys Pro Tyr Lys Gln Phe Lys Glu Met Leu
 435 440 445
 Glu Asn Phe Phe Ile Glu Ile Ala Arg Asp Phe Phe Lys Asp Asp Gly
 450 455 460
 Asp Met Ser Glu Leu Phe Val Glu Thr Lys Gln Arg Arg Asn Glu Glu
 465 470 475 480
 His Asp Leu Leu Ser Lys Arg Ser Lys Gln Thr Lys Ala Lys Lys Asp
 485 490 495
 Arg Leu Lys Lys Asp Leu Tyr Asp Phe Phe Asp Lys Leu Asp Asn Asp
 500 505 510
 Tyr Trp Asn Ile Glu Ile Asn Lys Leu Ile Asn Lys Asn Glu Glu Tyr
 515 520 525
 Phe Ser Ser Thr Glu Ile Thr Asp Thr Asn Ile Asp Tyr Val Tyr Asn
 530 535 540

Lys Ile Lys Glu Gln Asn Asp Ala Ile Ile Lys Asn Leu Arg Asn Ser
 545 550 555 560
 Val Asp Ile Lys Lys Pro Ser Gly Val Gly Leu Thr Lys Glu Leu Ser
 565 570 575
 Asn Leu Trp Asp Arg Tyr Gln Ile Glu Arg Gln Lys Ile Leu Leu Ser
 580 585 590
 Leu Asn Glu Leu Lys Asp Asn Val Asp Arg Lys Leu Ile Glu Leu Asp
 595 600 605
 Asn Lys Asn Asn Asp Phe Leu Asn Leu Arg Lys Arg Leu Glu Asp Ser
 610 615 620
 Leu Asn Leu Gln Gln Ser Tyr Tyr Glu Lys Glu Leu Thr Lys Leu Tyr
 625 630 635 640
 Asn Asp Ala Lys Asn Ala Leu Lys Asp Val Gln Ser Lys Ala Asn Arg
 645 650 655
 Leu Ile Ser Asp Asn Lys Lys Lys His Lys Ser Glu Leu Lys Asn Ile
 660 665 670
 Ser Tyr Glu Phe Gln Ser Thr Asn Leu Asn Gly Lys Asp Thr Ala Tyr
 675 680 685
 Ile Leu Asp Val Lys Arg Asn Leu Glu Ser Lys Ile Glu Asn Thr Ser
 690 695 700
 Asn Glu Val Ile Asn Glu Ile Arg Lys Leu Thr Asp Gln Ile Ala Ile
 705 710 715 720
 Ile Ser Asp Ser Thr Thr Ser Glu Asn Leu Ser Ser Ala Gln Val Thr
 725 730 735
 Glu Ala Ile Glu Thr Glu Leu Glu His Leu Arg Asp Gln Gln Ala Asn
 740 745 750
 Asn Ala Glu Leu Ile Leu Leu Gly Met Ala Leu Ser Val Val His His
 755 760 765
 Glu Phe Asn Gly Asn Ile Arg Ala Ile Arg Ser Ala Leu Arg Glu Leu
 770 775 780
 Lys Ala Trp Ala Asp Arg Asn Pro Lys Leu Asp Ile Ile Tyr Gln Lys
 785 790 795 800
 Ile Arg Thr Ser Phe Asp His Leu Asp Gly Tyr Leu Lys Thr Phe Thr
 805 810 815

Pro Leu Thr Arg Arg Leu Ser Arg Ser Lys Thr Asn Ile Thr Gly Thr
 820 825 830
 Ala Ile Leu Glu Phe Ile Arg Asp Val Phe Asp Asp Arg Leu Glu Lys
 835 840 845
 Glu Gly Ile Glu Leu Phe Thr Thr Ser Lys Phe Val Asn Gln Glu Ile
 850 855 860
 Val Thr Tyr Thr Ser Thr Ile Tyr Pro Val Phe Ile Asn Leu Ile Asp
 865 870 875 880
 Asn Ala Ile Tyr Trp Leu Gly Lys Thr Thr Gly Glu Lys Arg Leu Ile
 885 890 895
 Leu Asp Ala Thr Glu Thr Gly Phe Val Ile Gly Asp Thr Gly Pro Gly
 900 905 910
 Val Ser Thr Arg Asp Arg Asp Ile Ile Phe Asp Met Gly Phe Thr Arg
 915 920 925
 Lys Thr Gly Gly Arg Gly Met Gly Leu Phe Ile Ser Lys Glu Cys Leu
 930 935 940
 Ser Arg Asp Gly Phe Thr Ile Arg Leu Asp Asp Tyr Thr Pro Glu Gln
 945 950 955 960
 Gly Ala Phe Phe Ile Ile Glu Pro Ser Glu Glu Thr Ser Glu
 965 970

<210> 45

<211> 555

<212> PRT

<213> Escherichia coli

<400> 45

Met Thr Ser Ser Thr Asp Phe His Lys Leu Ser Glu Asp Cys Val Arg
 1 5 10 15
 Arg Phe Leu His Ser Val Val Ala Val Asp Asp Asn Met Ser Phe Gly
 20 25 30
 Ala Gly Ser Asp Thr Phe Pro Thr Asp Glu Asp Ile Asn Ala Leu Val
 35 40 45
 Asp Pro Asp Asp Asp Pro Thr Pro Ile Ile Thr Ala Ser Ala Ser Pro
 50 55 60
 Arg Ile Glu Ser Thr Lys Ser Lys Ala Lys Val Lys Asn His Pro Phe
 65 70 75 80

Asp Tyr Gln Ala Leu Ala Glu Ala Phe Ala Lys Asp Gly Ile Ala Cys
 85 90 95
 Cys Gly Leu Leu Ala Lys Ser Phe Asn Val Glu Glu Arg Asp Ile Ile
 100 105 110
 Thr Ala Ser Ser His Lys Ala Asp Ile Thr Ile Leu Asp Trp Asp Met
 115 120 125
 Gln Ser Asp Ser Gly Gln Phe Ala Ile Glu Ile Ile Lys Ser Ile Ile
 130 135 140
 Val Ser Asp Ile Asn Ser Gly Gly Arg Leu Arg Leu Leu Ser Ile Tyr
 145 150 155 160
 Thr Gly Glu His Val Thr Ala Val Ile Thr Lys Leu Asn Asn Glu Leu
 165 170 175
 Lys Lys Thr Tyr Arg Ser Val Ile Lys Asn Asp Asp Ser Ile Phe Ile
 180 185 190
 Glu Asp Asn Tyr Ala Leu Glu Gln Trp Cys Ile Val Val Ile Ser Lys
 195 200 205
 Asp Val Tyr Glu Lys Asp Leu Pro Asn Val Leu Ile Lys Lys Phe Thr
 210 215 220
 Asn Leu Thr Ala Gly Leu Leu Ser Asn Ala Ala Leu Ser Cys Ile Ser
 225 230 235 240
 Glu Ile Arg Glu Lys Thr His Gly Ile Leu Thr Lys Tyr Asn Asn Lys
 245 250 255
 Leu Asp Thr Ala Tyr Val Ser His Ile Leu Asn Leu Ile Lys Ser Lys
 260 265 270
 Glu Ser Arg Ala Tyr Ala Tyr Glu Asn Ala His Asp Tyr Ala Val Asp
 275 280 285
 Leu Ile Ser Glu Glu Ile Arg Ser Ile Leu Gln Ile Ser Glu Asn Leu
 290 295 300
 Lys Lys Ser Leu Ser Lys Asn Ser Leu Ser His Trp Pro Ile Phe His
 305 310 315 320
 Tyr Ala Lys Asn Gly Cys Lys Asn Phe Leu Leu Thr Gly Lys Lys Gln
 325 330 335
 Lys Asp Leu Ser Val Glu His Leu Arg Asn Ile Leu Ser Ala Asp Ser
 340 345 350

Leu Glu Glu Ile Gln His Ala Ile Glu His Ala Ser Leu Gly Lys Lys
 355 360 365
 Glu Tyr Leu Ser Gln Asp Gly Glu Glu Asp Lys Lys Leu Met Gln Leu
 370 375 380
 Cys Ser Leu Glu Ile Thr Arg Arg Ser Leu Arg Tyr His Ser His Ile
 385 390 395 400
 Asp Asn Val Ser Leu Lys Gln Gly Thr Leu Leu Leu Asp Ala Tyr Asn
 405 410 415
 Phe Val Tyr Leu Cys Ile Gln Pro Leu Cys Asp Ser Val Arg Leu His
 420 425 430
 Glu Lys Ala Asp Phe Leu Phe Leu Arg Gly Thr Leu Asp Asp Asn Asn
 435 440 445
 Tyr Asn Leu Leu Ile Glu Asp Glu Tyr Gly Gly Phe Tyr Lys Ile Lys
 450 455 460
 Met Pro Ala Lys Ala Ser Asn Ile Ile Ser Phe Ser Phe Gly Val Glu
 465 470 475 480
 Asn Gly Asn Gly Val Ile Ile Gly Lys Lys Asn Asn Leu Val Asn Thr
 485 490 495
 Asp Tyr Ile Ser Phe Val Pro Leu Leu Val Glu Lys Ile Ser Thr Pro
 500 505 510
 Lys Val Leu Lys Trp Ile Gly Glu Ile Lys Thr Thr Tyr Ala Gln Lys
 515 520 525
 Ile Thr Thr Asp Ile Val Ala Asn Leu Ser Arg Ile Gly Leu Asp Gln
 530 535 540
 His Glu Trp Leu Arg Ile Lys Ser Lys Asp Ile
 545 550 555

<210> 46

<211> 82

<212> PRT

<213> Escherichia coli

<400> 46

Met Ser Ser Arg Gln Ile Leu Glu His Tyr Asn Ala Leu Thr Tyr Pro
 1 5 10 15

Leu His Gln Ser Ile Leu Leu Gln Ile Met Thr Ser Asn Leu Leu Ser
 20 25 30

Val Cys Thr Gly Lys Ser Ile Tyr Glu Asp Ile Ser Gly Ser Ser Trp
 35 40 45

Asn Ile Ile His Phe Asn Ile Pro Leu Pro Ile Ser Arg Ala Arg Leu
 50 55 60

Ser Ile Phe Ser Tyr Cys Val Arg Ile Lys Pro Trp Met Ser Met Asp
 65 70 75 80

Tyr Met

<210> 47
 <211> 98
 <212> PRT
 <213> Escherichia coli

<400> 47
 Met Ser Ile Ile Phe Asn Gly His Tyr Arg Met Lys His Arg Thr Trp
 1 5 10 15

Ile Thr Glu Ala Leu Arg Leu His Phe Glu Glu His Leu Pro Gln Val
 20 25 30

Val Val Gly Arg Arg Leu Gly Val Pro Lys Ser Thr Ala Cys Gly Met
 35 40 45

Phe Val Arg Phe Arg Lys Ala Gly Phe Ser Trp Pro Leu Pro Ala Gly
 50 55 60

Met Ser Glu Arg Glu Leu Asp Gly Arg Leu Tyr Gly Ser Thr Ser Thr
 65 70 75 80

Val Pro Val Val Leu Cys Ser Gly Ser Val Ile Gln Asp Thr Ser Lys
 85 90 95

Ser Cys

<210> 48
 <211> 106
 <212> PRT
 <213> Escherichia coli

<400> 48
 Met Ile Lys Thr Arg Arg Thr Lys Arg Thr Phe Ser Pro Glu Phe Lys
 1 5 10 15

Leu Glu Ala Phe Glu Gln Val Val Val Lys Tyr Gln Arg Asp Val Arg
 20 25 30

Glu Val Ala Gln Ala Leu Glu Leu Asn Pro Asp His Leu Arg Lys Trp
 35 40 45
 Ile Arg Leu Tyr Lys Gln Glu Leu Gln Gly Ile Glu Pro Ala Gly Asn
 50 55 60
 Ala Ile Thr Pro Glu Gln Arg Glu Ile Gln Gln Leu Lys Ala Gln Ile
 65 70 75 80
 Lys Arg Val Glu Met Glu Lys Glu Ile Leu Lys Gln Ala Ala Val Leu
 85 90 95
 Met Ser Glu Ile Pro Gly Lys Leu Ser Arg
 100 105

<210> 49
 <211> 27
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:Oligonucleotide

<400> 49
 tgctctagag ccattactca gaatggg 27

<210> 50
 <211> 26
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:Oligonucleotide

<400> 50
 cgcgagctcg acgactgaat gatccc 26

<210> 51
 <211> 26
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:Oligonucleotide

<400> 51
 tccccgggt actgcagcac tcaacc 26

<210> 52
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Oligonucleotide

<400> 52
gatccccggga ccactgaaat gcgtgc 26

<210> 53
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Oligonucleotide

<400> 53
tcgtctagag atgatggtga tggagcg 27

<210> 54
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Oligonucleotide

<400> 54
gaactgcagc caaatactga taccaccc 28

<210> 55
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Oligonucleotide

<400> 55
gaactgcagg ctaaaacaga agacgcg 27

<210> 56
<211> 27

<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Oligonucleotide

<400> 56

catgcatgca ctccatatga caaccgc

27

<210> 57

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Oligonucleotide

<400> 57

tcgtctagaa tgaagctgcg catgagg

27

<210> 58

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Oligonucleotide

<400> 58

caactgcagt cgcaaattgc gaactgg

27

<210> 59

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Oligonucleotide

<400> 59

caactgcaga ccgcaacttt tcgacgc

27

<210> 60

<211> 27

<212> DNA

<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Oligonucleotide

<400> 60
catgcatgcc agtgagccat tgttccc 27

<210> 61
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Oligonucleotide

<400> 61
tgctctagat acgactctga caggagg 27

<210> 62
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Oligonucleotide

<400> 62
tcagatatca actaccagca gtttgg 26

<210> 63
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Oligonucleotide

<400> 63
tcagatatcc ataaagagtg acgtggc 27

<210> 64
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Oligonucleotide

<400> 64
tgctctagaa aacgtggcaa cagagcg 27

<210> 65
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Oligonucleotide

<400> 65
tgctctagaa ggcgttgctg atcctg 26

<210> 66
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Oligonucleotide

<400> 66
gaactgcagg aaaaggccga gcagactg 28

<210> 67
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Oligonucleotide

<400> 67
gaactgcagt acagccatgt ttacggt 27

<210> 68
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Oligonucleotide

<400> 68
catgcatgcg gtgtacgaca gtttgcg 27

<210> 69
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Oligonucleotide

<400> 69
tgctctagac acatcatggg cacacc 26

<210> 70
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Oligonucleotide

<400> 70
gaactgcaga accgtccaca tcaggcg 27

<210> 71
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Oligonucleotide

<400> 71
gaactgcaga ccctgcttgc cattccg 27

<210> 72
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Oligonucleotide

<400> 72
catgcatgca taagcgtcga acaggcg 27